

Package ‘mirt’

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Title Multidimensional Item Response Theory

Description Analysis of dichotomous and polytomous response data using unidimensional and multidimensional latent trait models under the Item Response Theory paradigm. Exploratory and confirmatory models can be estimated with quadrature (EM) or stochastic (MHRM) methods. Confirmatory bi-factor and two-tier analyses are available for modeling item testlets. Multiple group analysis and mixed effects designs also are available for detecting differential item functioning and modelling item and person covariates.

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mirt-package *Full information maximum likelihood estimation of IRT models.*

Description

Full information maximum likelihood estimation of multidimensional IRT models

Details

Analysis of dichotomous and polytomous response data using unidimensional and multidimensional latent trait models under the Item Response Theory paradigm. Exploratory and confirmatory models can be estimated with quadrature (EM) or stochastic (MHRM) methods. Confirmatory bi-factor and two-tier analyses are available for modeling item testlets. Multiple group analysis and mixed effects designs also are available for detecting differential item functioning and modeling item and person covariates.

Users interested in the most recent version of this package can visit <https://github.com/philchalmers/mirt> and follow the instructions for installing the package from source. Questions regarding the package can be sent to the *mirt-package* Google Group, located at <https://groups.google.com/forum/#!forum/mirt-package>.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

anova-method *Compare nested models*

Description

Compare nested models using likelihood ratio, AIC, BIC, etc.

Usage

```
## S4 method for signature 'ExploratoryClass'  
anova(object, object2, verbose = TRUE)
```

Arguments

object	an object of class ExploratoryClass, ConfirmatoryClass, MultipleGroupClass, or MixedClass
object2	a second model estimated from any of the mirt package estimation methods
verbose	logical; print additional information to console?

Examples

```
## Not run:
x <- mirt(Science, 1)
x2 <- mirt(Science, 2)
anova(x, x2)

## End(Not run)
```

bfactor

Full-Information Item Bi-factor and Two-Tier Analysis

Description

bfactor fits a confirmatory maximum likelihood two-tier/bifactor model to dichotomous and polytomous data under the item response theory paradigm. The IRT models are fit using a dimensional reduction EM algorithm so that regardless of the number of specific factors estimated the model only uses the number of factors in the second-tier structure plus 1. For the bifactor model the maximum number of dimensions is only 2 since the second-tier only consists of a ubiquitous unidimensional factor. See [mirt](#) for appropriate methods to be used on the objects returned from the estimation.

Usage

```
bfactor(data, model, model2 = mirt.model(paste0("G = 1-", ncol(data))),
        group = NULL, quadpts = 21, ...)
```

Arguments

data	a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
model	a numeric vector specifying which factor loads on which item. For example, if for a 4 item test with two specific factors, the first specific factor loads on the first two items and the second specific factor on the last two, then the vector is <code>c(1, 1, 2, 2)</code> . For items that should only load on the second-tier factors (have no specific component) NA values may be used as place-holders. These numbers will be translated into a format suitable for <code>mirt.model()</code> , combined with the definition in <code>model2</code> , with the letter 'S' added to the respective factor number
model2	a two-tier model specification object defined by <code>mirt.model()</code> . By default the model will fit a unidimensional model in the second-tier, and therefore be equivalent to the bifactor model

group	a factor variable indicating group membership used for multiple group analyses
quadpts	number of quadrature nodes to use. Default is 21
...	additional arguments to be passed to the estimation engine. See mirt for more details and examples

Details

bfactor follows the item factor analysis strategy explicated by Gibbons and Hedeker (1992), Gibbons et al. (2007), and Cai (2010). Nested models may be compared via an approximate chi-squared difference test or by a reduction in AIC or BIC (accessible via [anova](#)). See [mirt](#) for more details regarding the IRT estimation approach used in this package. The default is to use 21 quadrature for each dimensions, but this can be over-written by passing a `quadpts = #` argument.

Note: for multiple group two-tier analyses only the second-tier means and variances should be freed since the specific factors are not treated independently due to the dimension reduction technique.

Value

function returns an object of class `ConfirmatoryClass` ([ConfirmatoryClass-class](#)).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

- Cai, L. (2010). A two-tier full-information item factor analysis model with applications. *Psychometrika*, 75, 581-612.
- Chalmers, R., P. (2012). mirt: A Multidimensional Item Response Theory Package for the R Environment. *Journal of Statistical Software*, 48(6), 1-29.
- Gibbons, R. D., & Hedeker, D. R. (1992). Full-information Item Bi-Factor Analysis. *Psychometrika*, 57, 423-436.
- Gibbons, R. D., Darrell, R. B., Hedeker, D., Weiss, D. J., Segawa, E., Bhaumik, D. K., Kupfer, D. J., Frank, E., Grochocinski, V. J., & Stover, A. (2007). Full-Information item bifactor analysis of graded response data. *Applied Psychological Measurement*, 31, 4-19.

See Also

[mirt](#)

Examples

```
## Not run:

###load SAT12 and compute bifactor model with 3 specific factors
data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
specific <- c(2,3,2,3,3,2,1,2,1,1,1,3,1,3,1,2,1,1,3,3,1,1,3,1,1,3,3,1,3,2,3,1,2)
mod1 <- bfactor(data, specific)
```

```

summary(mod1)
itemplot(mod1, 18, drop.zeros = TRUE) #drop the zero slopes to allow plotting

###Try with fixed guessing parameters added
guess <- rep(.1,32)
mod2 <- bfactor(data, specific, guess = guess)
coef(mod2)
anova(mod1, mod2)

## don't estimate specific factor for item 32
specific[32] <- NA
mod3 <- bfactor(data, specific)
anova(mod1, mod3)

# same, but decalred manually (not run)
#sv <- mod2values(mod1)
#sv$value[220] <- 0 #parameter 220 is the 32 items specific slope
#sv$est[220] <- FALSE
#mod3 <- bfactor(data, specific, pars = sv) #with excellent starting values

#####
# mixed itemtype example

#simulate data
a <- matrix(c(
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,0.5,NA,
1,NA,0.5,
1,NA,0.5,
1,NA,0.5,
1,NA,0.5,
1,NA,0.5,
1,NA,0.5,
1,NA,0.5),ncol=3,byrow=TRUE)

d <- matrix(c(
-1.0,NA,NA,
-1.5,NA,NA,
1.5,NA,NA,
0.0,NA,NA,
2.5,1.0,-1,
3.0,2.0,-0.5,
3.0,2.0,-0.5,
3.0,2.0,-0.5,
2.5,1.0,-1,
2.0,0.0,NA,
-1.0,NA,NA,

```

```

-1.5,NA,NA,
 1.5,NA,NA,
 0.0,NA,NA),ncol=3,byrow=TRUE)
items <- rep('dich', 14)
items[5:10] <- 'graded'

sigma <- diag(3)
dataset <- simdata(a,d,2000,itemtype=items,sigma=sigma)

specific <- c(rep(1,7),rep(2,7))
simmod <- bfactor(dataset, specific)
coef(simmod)

#####
# Two-tier model

#simulate data
set.seed(1234)
a <- matrix(c(
0,1,0.5,NA,NA,
0,1,0.5,NA,NA,
0,1,0.5,NA,NA,
0,1,0.5,NA,NA,
0,1,0.5,NA,NA,
0,1,NA,0.5,NA,
0,1,NA,0.5,NA,
0,1,NA,0.5,NA,
1,0,NA,0.5,NA,
1,0,NA,0.5,NA,
1,0,NA,NA,0.5,
1,0,NA,NA,0.5,
1,0,NA,NA,0.5,
1,0,NA,NA,0.5),ncol=5,byrow=TRUE)

d <- matrix(rnorm(16))
items <- rep('dich', 16)

sigma <- diag(5)
sigma[1,2] <- sigma[2,1] <- .4
dataset <- simdata(a,d,2000,itemtype=items,sigma=sigma)

specific <- c(rep(1,5),rep(2,6),rep(3,5))
model <- mirt.model('
  G1 = 1-8
  G2 = 9-16
  COV = G1*G2')

#quadpts dropped for faster estimation, but not as precise
simmod <- bfactor(dataset, specific, model, quadpts = 9, TOL = 1e-3)
coef(simmod)
summary(simmod)

```

```
## End(Not run)
```

Bock1997

Description of Bock 1997 data

Description

A 3-item tabulated data set extracted from Table 3 in Chapter Two.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Bock, R. D. (1997). The Nominal Categories Model. In van der Linden, W. J. & Hambleton, R. K. *Handbook of modern item response theory*. New York: Springer.

Examples

```
## Not run:
dat <- expand.table(Bock1997)
head(dat)
mod <- mirt(dat, 1, 'nominal')

#reproduce table 3 in Bock (1997)
fs <- round(fscores(mod, verbose = FALSE)[,c('F1', 'SE_F1')], 2)
fttd <- residuals(mod, type = 'exp')
table <- data.frame(fttd[, -ncol(fttd)], fs)
table

#using nominal.highlow matrix to specify lowest and highest categories
(nominal.highlow <- matrix(c(4,4,4,4,1,1,1,1), 2, byrow = TRUE))
mod <- mirt(dat, 1, 'nominal', nominal.highlow=nominal.highlow)
coef(mod)

## End(Not run)
```

boot.mirt	<i>Calculate bootstrapped standard errors for estimated models</i>
-----------	--

Description

Given an internal mirt object estimate the bootstrapped standard errors. It may be beneficial to run the computations using multi-core architecture (e.g., the `parallel` package).

Usage

```
boot.mirt(x, R = 100, ...)
```

Arguments

x	an estimated object from <code>mirt</code> , <code>bfactor</code> , or <code>multipleGroup</code>
R	number of draws to use (passed to the <code>boot()</code> function)
...	additional arguments to be passed on to <code>boot(...)</code>

See Also

[PLCI.mirt](#)

Examples

```
## Not run:  
  
#standard  
mod <- mirt(Science, 1)  
booted <- boot.mirt(mod)  
plot(booted)  
booted  
  
#run in parallel using snow back-end using all available cores  
mod <- mirt(Science, 1)  
booted <- boot.mirt(mod, parallel = 'snow', ncpus = parallel::detectCores())  
booted  
  
## End(Not run)
```

coef-method

*Extract raw coefs from model object***Description**

Return a list (or data.frame) of raw item and group level coefficients.

Usage

```
## S4 method for signature 'ExploratoryClass'
coef(object, CI = 0.95, printSE = FALSE,
      rotate = "", Target = NULL, digits = 3, IRTpars = FALSE,
      rawug = FALSE, as.data.frame = FALSE, verbose = TRUE, ...)
```

Arguments

object	an object of class ExploratoryClass, ConfirmatoryClass, MultipleGroupClass, or MixedClass
CI	the amount of converged used to compute confidence intervals; default is 95 percent confidence intervals
IRTpars	logical; convert slope intercept parameters into traditional IRT parameters? Only applicable to unidimensional models
rotate	see mirt for details
Target	a dummy variable matrix indicting a target rotation pattern
printSE	logical; print the standard errors instead of the confidence intervals?
digits	number of significant digits to be rounded
as.data.frame	logical; convert list output to a data.frame instead?
verbose	logical; allow information to be printed to the console?
rawug	logical; return the untransformed internal g and u parameters? If FALSE, g and u's are converted with the original format along with delta standard errors
...	additional arguments to be passed

See Also

[summary-method](#)

Examples

```
## Not run:
dat <- expand.table(LSAT7)
x <- mirt(dat, 1)
coef(x)
coef(x, IRTpars = TRUE)

#with computed information matrix
```

```

x <- mirt(dat, 1, SE = TRUE)
coef(x)
coef(x, printSE = TRUE)
coef(x, as.data.frame = TRUE)

#two factors
x2 <- mirt(Science, 2)
coef(x2)
coef(x2, rotate = 'varimax')

## End(Not run)

```

ConfirmatoryClass-class

Class "ConfirmatoryClass"

Description

Defines the object returned from `bfactor` and `mirt` when the estimated model is confirmatory.

Slots

Data: Object of class "list", contains various data matrices and properties
iter: Object of class "numeric", number of iterations
pars: Object of class "list", estimated parameter objects list
shortpars: Object of class "numeric", unique estimated parameters
model: Object of class "list", list containing original model
K: Object of class "numeric", number of item categories
itemloc: Object of class "numeric", index for tabdata
df: Object of class "numeric", degrees of freedom
AIC: Object of class "numeric", Akaike's information criteria
BIC: Object of class "numeric", Bayesian information criteria
G2: Object of class "numeric", G squared stat
p: Object of class "numeric", p-value for G2
df: Object of class "numeric", degrees of freedom
RMSEA: Object of class "numeric", root mean-square error of approximation for G2
TLI: Object of class "numeric", Tucker-Lewis index for G2
CFI: Object of class "numeric", CFI for G2
logLik: Object of class "numeric", observed log-likelihood
SElogLik: Object of class "numeric", Monte Carlo standard error for log-likelihood
F: Object of class "matrix", unrotated factor loadings

h2: Object of class "numeric", commonalities
Theta: Object of class "matrix", ability grid
P1: Object of class "numeric", normed likelihoods for tabulated response
Prior: Object of class "list", prior distribution used during estimation. Empty unless empiricalhist = TRUE
prodlist: Object of class "list", list containing product combination of factors
converge: Object of class "numeric", convergence diagnostic
quadpts: Object of class "numeric", number of quadrature points
esttype: Object of class "character", indicates whether estimation was 'EM' or 'MHRM'
random: Object of class "list", typically null, except for internal mixed model usage
null.mod: Object of class "ExploratoryClass", null model
condnum: Object of class "numeric", condition number of information matrix
bfactor: Object of class "list", contains information from bfactor() estimation
secondordertest: Object of class "logical", indicate whether information matrix passes second-order test
infomethod: Object of class "character", indicates which information estimation method was used
TOL: Object of class "numeric", tolerance stopping criteria
CUSTOM.IND: Object of class "integer", an internal index
SLOW.IND: Object of class "integer", an internal index
Call: Object of class "call", call

Methods

coef signature(object = "ConfirmatoryClass")
print signature(x = "ConfirmatoryClass")
residuals signature(object = "ConfirmatoryClass")
show signature(object = "ConfirmatoryClass")
summary signature(object = "ConfirmatoryClass")
logLik signature(object = "ConfirmatoryClass")
anova signature(object = "ConfirmatoryClass")

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

 createItem

Create a user defined item with correct generic functions

Description

Initializes the proper S4 class and methods necessary for mirt functions to use in estimation. To use the defined objects pass to the `mirt(..., customItems = list())` command, and ensure that the classes are properly labeled and unique in the list.

Usage

```
createItem(name, par, est, P, gr = NULL, hss = NULL, lbound = NULL,
           ubound = NULL)
```

Arguments

name	a character indicating the item class name to be defined
par	a named vector of the starting values for the parameters
est	a logical vector indicating which parameters should be freely estimated by default
P	the probability trace function for all categories (first column is category 1, second category two, etc). First input contains a vector of all the item parameters, the second input must be a matrix called Theta, and the third input must be the number of categories called ncat. Function also must return a matrix object of category probabilities
gr	gradient function (vector of first derivatives) of the log-likelihood used in estimation. The function must be of the form <code>gr(x, Theta)</code> , where <code>x</code> is the object defined by <code>createItem()</code> and <code>Theta</code> is a matrix of latent trait parameters. Tabulated (EM) or raw (MHRM) data are located in the <code>x@dat</code> slot, and are used to form the complete data log-likelihood. If not specified a numeric approximation will be used
hss	Hessian function (matrix of second derivatives) of the log-likelihood used in estimation. If not specified a numeric approximation will be used (required for the MH-RM algorithm only). The input is identical to the <code>gr</code> argument
lbound	optional vector indicating the lower bounds of the parameters. If not specified then the bounds will be set to <code>-Inf</code>
ubound	optional vector indicating the lower bounds of the parameters. If not specified then the bounds will be set to <code>Inf</code>

Details

The `summary()` function will not return proper standardized loadings since the function is not sure how to handle them (no slopes could be defined at all!). Instead loadings of .001 are filled in as place-holders.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:

name <- 'old2PL'
par <- c(a = .5, b = -2)
est <- c(TRUE, TRUE)
P.old2PL <- function(par,Theta, ncat){
  a <- par[1]
  b <- par[2]
  P1 <- 1 / (1 + exp(-1*a*(Theta - b)))
  cbind(1-P1, P1)
}

x <- createItem(name, par=par, est=est, P=P.old2PL)

#So, let's estimate it!
dat <- expand.table(LSAT7)
sv <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x), pars = 'values')
tail(sv) #looks good
mod <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x), verbose = TRUE)
coef(mod)
mod2 <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x),
  verbose = TRUE, method = 'MHRM')
coef(mod2)

###non-linear
name <- 'nonlin'
par <- c(a1 = .5, a2 = .1, d = 0)
est <- c(TRUE, TRUE, TRUE)
P.nonlin <- function(par,Theta, ncat=2){
  a1 <- par[1]
  a2 <- par[2]
  d <- par[3]
  P1 <- 1 / (1 + exp(-1*(a1*Theta + a2*Theta^2 + d)))
  cbind(1-P1, P1)
}

x2 <- createItem(name, par=par, est=est, P=P.nonlin)

mod <- mirt(dat, 1, c(rep('2PL',4), 'nonlin'), customItems=list(nonlin=x2), verbose = TRUE)
coef(mod)

###nominal response model (Bock 1972 version)
Tnom.dev <- function(ncat) {
  T <- matrix(1/ncat, ncat, ncat - 1)
  diag(T[-1, ]) <- diag(T[-1, ]) - 1
  return(T)
}
```

```

name <- 'nom'
par <- c(alp=c(3,0,-3),gam=rep(.4,3))
est <- rep(TRUE, length(par))
P.nom <- function(par, Theta, ncat){
  alp <- par[1:(ncat-1)]
  gam <- par[ncat:length(par)]
  a <- Tnom.dev(ncat) %%% alp
  c <- Tnom.dev(ncat) %%% gam
  z <- matrix(0, nrow(Theta), ncat)
  for(i in 1:ncat)
    z[,i] <- a[i] * Theta + c[i]
  P <- exp(z) / rowSums(exp(z))
  P
}

nom1 <- createItem(name, par=par, est=est, P=P.nom)
nommod <- mirt(Science, 1, 'nom1', customItems=list(nom1=nom1))
coef(nommod)
Tnom.dev(4) %%% coef(nommod)[[1]][1:3] #a
Tnom.dev(4) %%% coef(nommod)[[1]][4:6] #d

## End(Not run)

```

deAyala

Description of deAyala data

Description

Mathematics data from de Ayala (2009; pg. 14); 5 item dataset in table format.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

de Ayala, R. J. (2009). *The theory and practice of item response theory*. Guilford Press.

Examples

```

## Not run:
dat <- expand.table(deAyala)
head(dat)

## End(Not run)

```

Description

This function runs the Wald and likelihood-ratio approaches for testing differential item functioning (DIF). This is primarily a convenience wrapper to the `multipleGroup` function for performing standard DIF procedures. Models can be estimated in parallel automatically by defining a parallel object with `mirtCluster`, which will help to decrease the runtime.

Usage

```
DIF(MGmodel, which.par, scheme = "add",
    items2test = 1:ncol(MGmodel@Data$data), seq_stat = "SABIC",
    Wald = FALSE, p.adjust = "none", max_run = Inf, plotdif = FALSE,
    type = "trace", verbose = TRUE, ...)
```

Arguments

<code>MGmodel</code>	an object returned from <code>multipleGroup</code> to be used as the reference model
<code>which.par</code>	a character vector containing the parameter names which will be inspected for DIF
<code>Wald</code>	logical; perform Wald tests for DIF instead of likelihood ratio test?
<code>items2test</code>	a numeric vector, or character vector containing the item names, indicating which items will be tested for DIF. In models where anchor items are known, omit them from this vector. For example, if items 1 and 2 are anchors in a 10 item test, then <code>items2test = 3:10</code> would work for testing the remaining items (important to remember when using sequential schemes)
<code>scheme</code>	type of DIF analysis to perform, either by adding or dropping constraints across groups. These can be: <ul style="list-style-type: none"> 'add' parameters in <code>which.par</code> will be constrained each item one at a time for items that are specified in <code>items2test</code>. This is beneficial when examining DIF from a model with parameters freely estimated across groups, and when inspecting differences via the Wald test 'drop' parameters in <code>which.par</code> will be freely estimated for items that are specified in <code>items2test</code>. This is useful when supplying an overly restrictive model and attempting to detect DIF with a slightly less restrictive model 'add_sequential' sequentially loop over the items being tested, and at the end of the loop treat DIF tests that satisfy the <code>seq_stat</code> criteria as invariant. The loop is then re-run on the remaining invariant items to determine if they are now displaying DIF in the less constrained model, and when no new invariant item is found the algorithm stops and returns the items that displayed DIF

	'drop_sequential' sequentially loop over the items being tested, and at the end of the loop treat items that violate the seq_stat criteria as demonstrating DIF. The loop is then re-run, leaving the items that previously demonstrated DIF as variable across groups, and the remaining test items that previously showed invariance are re-tested. The algorithm stops when no more items showing DIF are found and returns the items that displayed DIF
seq_stat	select a statistic to test for in the sequential schemes. Potential values are (in descending order of power) 'AIC', 'AICc', 'SABIC', and 'BIC'. If a numeric value is input that ranges between 0 and 1, the 'p' value will be tested (e.g., seq_stat = .05 will test for the difference of $p < .05$ in the add scheme, or $p > .05$ in the drop scheme), along with the specified p.adjust input
max_run	a number indicating the maximum number of cycles to perform in sequential searches. The default is to perform search until no further DIF is found
plotdif	logical; create itemplots for items that are displaying DIF according to the seq_stat criteria? Only available for 'add' type schemes
type	the type of plot argument passed to plot(). Default is 'trace', though another good option is 'infotrace'. For ease of viewing, the facet_item argument to mirt's plot() function is set to TRUE
p.adjust	string to be passed to the p.adjust function to adjust p-values. Adjustments are located in the adj_pvals element in the returned list
verbose	logical print extra information to the console?
...	additional arguments to be passed to multipleGroup and plot

Author(s)

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See Also

[multipleGroup](#)

Examples

```
## Not run:

#simulate data where group 2 has a smaller slopes and more extreme intercepts
set.seed(12345)
a1 <- a2 <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d1 <- d2 <- matrix(rnorm(15,0,.7),ncol=1)
a2[1:2, ] <- a1[1:2, ]/3
d1[c(1,3), ] <- d2[c(1,3), ]/4
head(data.frame(a.group1 = a1, a.group2 = a2, d.group1 = d1, d.group2 = d2))
itemtype <- rep('dich', nrow(a1))
N <- 1000
dataset1 <- simdata(a1, d1, N, itemtype)
dataset2 <- simdata(a2, d2, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
```

```

#### no anchors, all items tested for DIF by adding item constrains one item at a time.
# define a parallel cluster (optional) to help speed up internal functions
mirtCluster()

# Information matrix with crossprod
model <- multipleGroup(dat, 1, group, SE = TRUE)

#test whether adding slopes and intercepts constrains results in DIF. Plot items showing DIF
resulta1d <- DIF(model, c('a1', 'd'), plotdif = TRUE)
resulta1d

#same as above, but using Wald tests with Benjamini & Hochberg adjustment
resulta1dWald <- DIF(model, c('a1', 'd'), Wald = TRUE, p.adjust = 'fdr')
resulta1dWald
round(resulta1dWald$adj_pvals, 4)

#test whether adding only slope constraints results in DIF for all items
resulta1 <- DIF(model, 'a1')
resulta1

#following up on resulta1d, to determine whether it's a1 or d parameter causing DIF
(a1s <- DIF(model, 'a1', items2test = 1:3))
(ds <- DIF(model, 'd', items2test = 1:3))

#### using items 4 to 15 as anchors
itemnames <- colnames(dat)
model_anchor <- multipleGroup(dat, model = 1, group = group,
  invariance = c(itemnames[4:15], 'free_means', 'free_var'))
anchor <- DIF(model_anchor, c('a1', 'd'), items2test = 1:3)
anchor

### drop down approach (freely estimating parameters accross groups) when
### specifying a highly constrained model with estimated latent parameters
model_constrained <- multipleGroup(dat, 1, group,
  invariance = c(colnames(dat), 'free_means', 'free_var'))
dropdown <- DIF(model_constrained, 'd', scheme = 'drop')
dropdown

### sequential searches using SABIC as the selection criteria
# starting from completely different models
model <- multipleGroup(dat, 1, group)
stepup <- DIF(model, c('a1', 'd'), scheme = 'add_sequential')
stepup

#step down procedure for highly constrained model
model <- multipleGroup(dat, 1, group, invariance = itemnames)
stepdown <- DIF(model, c('a1', 'd'), scheme = 'drop_sequential')
stepdown

## End(Not run)

```

DTF

*Differential test functioning***Description**

THIS FUNCTION IS CURRENTLY EXPERIMENTAL.

Usage

```
DTF(mod, MI = NULL, CI = 0.95, npts = 1000, theta_lim = c(-6, 6),
    Theta_nodes = NULL, plot = FALSE, auto.key = TRUE, ...)
```

Arguments

mod	a multipleGroup object which estimated only 2 groups
MI	a number indicating how many draws to take to form a suitable multiple imputation for the expected test scores (100 or more). Requires an estimated parameter information matrix. Returns a list containing the bootstrap distribution and null hypothesis test for the sDTF statistic
CI	range of confidence interval when using MI input
npts	number of points to use in the integration. Default is 1000
theta_lim	lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with npts
Theta_nodes	an optional matrix of Theta values to be evaluated in the MI draws for the sDTF statistic. However, these values are not averaged across, and instead give the bootstrap confidence intervals at the respective Theta nodes. Useful when following up a large uDTF/sDTF statistic to determine where the difference between the test curves are large (while still accounting for sampling variability). Returns a matrix with observed variability
plot	logical; plot the test score functions with imputed confidence envelopes?
auto.key	logical; automatically generate key in lattice plot?
...	additional arguments to be passed to lattice

Details

Function performs various omnibus differential test functioning procedures on an object estimated with `multipleGroup()`. If the latent means/covariances are suspected to differ then the input object should contain a set of 'anchor' items to ensure that only differential test features are being detected rather than group differences. Returns signed (average area above and below) and unsigned (total area) statistics, with descriptives such as the percent average bias between group total scores for each statistic.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

See Also

[multipleGroup](#), [DIF](#)

Examples

```
## Not run:
set.seed(1234)
n <- 30
N <- 500

# only first 5 items as anchors
model <- mirt.model('F = 1-30
                   CONSTRAINTB = (1-5, a1), (1-5, d)')

a <- matrix(1, n)
d <- matrix(rnorm(n), n)
group <- c(rep('G1', N), rep('G2', N))

## -----
# groups completely equal
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a, d, N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE, SE.type='crossprod',
                    invariance=c('free_means', 'free_var'))
plot(mod, type = 'score')

DTF(mod)
mirtCluster()
DTF(mod, MI = 1000) #95% C.I. for sDTI containing 0. uDTF is very small

## -----
## random slopes and intercepts for 15 items, and latent mean difference
## (no systematic DTF should exist, but DIF will be present)
dat1 <- simdata(a, d, N, itemtype = 'dich', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), sign(rnorm(n-15))*runif(n-15, .25, .5)),
               d + c(numeric(15), sign(rnorm(n-15))*runif(n-15, .5, 1)), N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod1 <- multipleGroup(dat, 1, group=group)
plot(mod1, type = 'score') #does not account for group differences! Need anchors

mod2 <- multipleGroup(dat, model, group=group, SE=TRUE, SE.type = 'crossprod',
                    invariance=c('free_means', 'free_var'))
plot(mod2, type = 'score')

#significant DIF in multiple items...
DIF(mod2, which.par=c('a1', 'd'), items2test=16:30)
DTF(mod2)
DTF(mod2, MI=1000)

## -----
## systematic differing slopes and intercepts (clear DTF)
```

```

dat1 <- simdata(a, d, N, itemtype = 'dich', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), rnorm(n-15, 1, .25)), d + c(numeric(15), rnorm(n-15, 1, .5)),
               N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod3 <- multipleGroup(dat, model, group=group, SE=TRUE, SE.type='crossprod',
                    invariance=c('free_means', 'free_var'))
plot(mod3, type = 'score') #visable DTF happening

DIF(mod3, c('a1', 'd'), items2test=16:30)
DTF(mod3) #unsigned bias. Signed bias indicates group 2 scores generally lower
DTF(mod3, MI=1000)
DTF(mod3, MI=1000, plot=TRUE)

## End(Not run)

```

expand.table

Expand summary table of patterns and frequencies

Description

The `expand.table` function expands a summary table of unique response patterns to a full sized data-set. The response frequencies must be on the rightmost column of the input data.

Usage

```
expand.table(tabdata)
```

Arguments

`tabdata` An object of class `data.frame`, `matrix`, or `table` with the unique response patterns and the number of frequencies in the rightmost column.

Value

Returns a numeric matrix with all the response patterns.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```

## Not run:
data(LSAT7)
LSAT7full <- expand.table(LSAT7)

## End(Not run)

```

expected.item	<i>Function to calculate expected value of item</i>
---------------	---

Description

Given an internal mirt object extracted from an estimated model compute the expected value for an item given the ability parameter(s).

Usage

```
expected.item(x, Theta, min = 0)
```

Arguments

x	an extracted internal mirt object containing item information
Theta	a vector (unidimensional) or matrix (multidimensional) of latent trait values
min	a constant value added to the expected values indicating the lowest theoretical category. Default is 0

See Also

[extract.item](#), [expected.test](#)

Examples

```
## Not run:
mod <- mirt(Science, 1)
extr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-6,6, length.out=200))
expected <- expected.item(extr.2, Theta, min(Science[,1])) #min() of first item
head(data.frame(expected, Theta=Theta))

## End(Not run)
```

expected.test	<i>Function to calculate expected test score</i>
---------------	--

Description

Given an estimated model compute the expected test score. Returns the expected values in the same form as the data used to estimate the model.

Usage

```
expected.test(x, Theta, group = NULL, mins = TRUE)
```

Arguments

x	an estimated mirt object
Theta	a matrix of latent trait values
group	a number signifying which group the item should be extracted from (applies to 'MultipleGroupClass' objects only)
mins	logical; include the minimum value constants in the dataset. If FALSE, the expected values for each item are determined from the scoring 0:(ncat-1)

See Also

[expected.item](#)

Examples

```
## Not run:
dat <- expand.table(deAyala)
model <- mirt.model('F = 1-5
                    CONSTRAIN = (1-5, a1)')
mod <- mirt(dat, model)

Theta <- matrix(seq(-6,6,.01))
tscore <- expected.test(mod, Theta)
tail(cbind(Theta, tscore))

## End(Not run)
```

ExploratoryClass-class

Class "ExploratoryClass"

Description

Defines the object returned from `mirt` when model is exploratory.

Slots

Data: Object of class "list", contains various data matrices and properties
iter: Object of class "numeric", number of iterations
pars: Object of class "list", estimated parameter objects list
shortpars: Object of class "numeric", unique estimated parameters
model: Object of class "list", list containing original model
K: Object of class "numeric", number of item categories
itemloc: Object of class "numeric", index for tabdata
AIC: Object of class "numeric", Akaike's information criteria

BIC: Object of class "numeric", Bayesian information criteria
G2: Object of class "numeric", G squared stat
p: Object of class "numeric", p-value for G2
df: Object of class "numeric", degrees of freedom
RMSEA: Object of class "numeric", root mean-square error of approximation for G2
TLI: Object of class "numeric", Tucker-Lewis index for G2
CFI: Object of class "numeric", CFI for G2
logLik: Object of class "numeric", observed log-likelihood
SElogLik: Object of class "numeric", Monte Carlo standard error for log-likelihood
F: Object of class "matrix", unrotated factor loadings
h2: Object of class "numeric", commonalities
Theta: Object of class "matrix", ability grid
P1: Object of class "numeric", normed likelihoods for tabulated response
prodlist: Object of class "list", list containing product combination of factors
rotate: Object of class "character", type of rotation to be used in summary
converge: Object of class "numeric", convergence diagnostic
quadpts: Object of class "numeric", number of quadrature points
eststype: Object of class "character", indicates whether estimation was 'EM' or 'MHRM'
null.mod: Object of class "ExploratoryClass", null model
Target: Object of class "numeric", dummy rotation matrix
condnum: Object of class "numeric", condition number of information matrix
secondordertest: Object of class "logical", indicate whether information matrix passes second-order test
bfactor: Object of class "list", an empty list
infomethod: Object of class "character", indicates which information estimation method was used
TOL: Object of class "numeric", tolerance stopping criteria
CUSTOM.IND: Object of class "integer", an internal index
SLOW.IND: Object of class "integer", an internal index
Call: Object of class "call", call

Methods

anova signature(object = "ExploratoryClass")
coef signature(object = "ExploratoryClass")
plot signature(x = "ExploratoryClass", y = "missing")
print signature(x = "ExploratoryClass")
residuals signature(object = "ExploratoryClass")
show signature(object = "ExploratoryClass")
summary signature(object = "ExploratoryClass")

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

extract.group *Extract a group from a multiple group mirt object*

Description

Extract a single group from an object defined by [multipleGroup](#).

Usage

```
extract.group(x, group)
```

Arguments

x	mirt model of class 'MultipleGroupClass'
group	a number signifying which group should be extracted

See Also

[extract.item](#)

Examples

```
## Not run:
#' set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('dich', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
models <- mirt.model('F1 = 1-15')

mod_configural <- multipleGroup(dat, models, group = group)
group.1 <- extract.group(mod_configural, 1) #extract first group
summary(group.1)
plot(group.1, type = 'score')

## End(Not run)
```

extract.item	<i>Extract an item object from mirt objects</i>
--------------	---

Description

Extract the internal mirt objects from any estimated model.

Usage

```
extract.item(x, item, group = NULL, drop.zeros = FALSE)
```

Arguments

x	mirt model of class 'ExploratoryClass', 'ConfirmatoryClass', or 'MultipleGroupClass'
item	a number or character signifying which item to extract
group	a number signifying which group the item should be extracted from (applies to 'MultipleGroupClass' only)
drop.zeros	logical; drop slope values that are numerically close to zero to reduce dimensionality? Useful in objects returned from bfactor or other confirmatory models that contain several zero slopes

See Also

[extract.group](#)

Examples

```
## Not run:
mod <- mirt(Science, 1)
extr.1 <- extract.item(mod, 1)

## End(Not run)
```

fscores	<i>Methods for Function fscores</i>
---------	-------------------------------------

Description

Computes MAP, EAP, ML (Embretson & Reise, 2000), EAP for sum-scores (Thissen et al., 1995), or WLE (Warm, 1989) factor scores with a multivariate normal prior distribution using equally spaced quadrature. EAP scores for models with more than three factors are generally not recommended since the integration grid becomes very large, resulting in slower estimation and less precision if the quadpts are too low. Therefore, MAP scores should be used instead of EAP scores for higher dimensional models. Multiple imputation variants are possible for each estimator if a parameter information matrix was computed, which are useful if the sample size/number of items were small.

Usage

```
fscores(object, rotate = "", full.scores = FALSE, method = "EAP",
        quadpts = NULL, response.pattern = NULL, returnER = FALSE,
        return.acov = FALSE, mean = NULL, cov = NULL, verbose = TRUE,
        scores.only = TRUE, full.scores.SE = FALSE, theta_lim = c(-6, 6),
        MI = 0, ...)
```

Arguments

<code>object</code>	a computed model object of class <code>ExploratoryClass</code> , <code>ConfirmatoryClass</code> , or <code>MultipleGroupClass</code>
<code>full.scores</code>	if <code>FALSE</code> (default) then a summary table with factor scores for each unique pattern is displayed. Otherwise the original data matrix is returned with the computed factor scores appended to the rightmost column
<code>rotate</code>	rotation declaration to be used when estimating the factor scores. If <code>""</code> then the <code>object@rotate</code> default value is used (only applicable to <code>ExploratoryClass</code> objects)
<code>method</code>	type of factor score estimation method. Can be expected a-posteriori (" <code>EAP</code> "), Bayes modal (" <code>MAP</code> "), weighted likelihood estimation (" <code>WLE</code> "), maximum likelihood (" <code>ML</code> "), or expected a-posteriori for sum scores (" <code>EAPsum</code> ")
<code>quadpts</code>	number of quadratures to use per dimension. If not specified, a suitable one will be created which decreases as the number of dimensions increases (and therefore for estimates such as <code>EAP</code> , will be less accurate). This is determined from the switch statement <code>quadpts <- switch(as.character(nfact), '1'=61, '2'=31, '3'=15, '4'=9, '5'=5, '6'=3, '7'=2, '8'=1, '9'=1, '10'=1)</code>
<code>theta_lim</code>	lower and upper range to evaluate latent trait integral for each dimension
<code>mean</code>	a vector for custom latent variable means. If <code>NULL</code> , the default for 'group' values from the computed mirt object will be used
<code>cov</code>	a custom matrix of the latent variable covariance matrix. If <code>NULL</code> , the default for 'group' values from the computed mirt object will be used
<code>MI</code>	a number indicating how many multiple imputation draws to perform. Default is 0, indicating that no MI draws will be performed
<code>response.pattern</code>	an optional argument used to calculate the factor scores and standard errors for a given response vector or matrix/data.frame
<code>returnER</code>	logical; return empirical reliability (also known as marginal reliability) estimates as a numeric values?
<code>return.acov</code>	logical; return a list containing covariance matrices instead of factors scores? <code>impute = TRUE</code> not supported with this option
<code>full.scores.SE</code>	logical; when <code>full.scores == TRUE</code> , also return the standard errors associated with each respondent? Default is <code>FALSE</code>
<code>verbose</code>	logical; print verbose output messages?
<code>scores.only</code>	logical; return only the factor scores (only applicable when <code>full.scores = TRUE</code>)
<code>...</code>	additional arguments

Details

The function will return either a table with the computed scores and standard errors, the original data matrix with scores appended to the rightmost column, or the scores only. By default the latent means and covariances are determined from the estimated object, though these can be overwritten. Iterative estimation methods can be estimated in parallel to decrease estimation times if a `mirtCluster` object is available.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

- Embretson, S. E. & Reise, S. P. (2000). *Item Response Theory for Psychologists*. Erlbaum.
- Thissen, D., Pommerich, M., Billeaud, K., & Williams, V. S. L. (1995). Item Response Theory for Scores on Tests Including Polytomous Items with Ordered Responses. *Applied Psychological Measurement, 19*, 39-49.
- Warm, T. A. (1989). Weighted likelihood estimation of ability in item response theory. *Psychometrika, 54*, 427-450.

Examples

```
## Not run:

mod <- mirt(Science, 1)
tabscores <- fscores(mod)
head(tabscores)
fullscores <- fscores(mod, full.scores = TRUE)
fullscores_with_SE <- fscores(mod, full.scores = TRUE, full.scores.SE=TRUE)
head(fullscores)
head(fullscores_with_SE)

#change method argument to use MAP estimates
fullscores <- fscores(mod, full.scores = TRUE, method='MAP')
head(fullscores)

#calculate MAP for a given response vector
fscores(mod, method='MAP', response.pattern = c(1,2,3,4))
#or matrix
fscores(mod, method='MAP', response.pattern = rbind(c(1,2,3,4), c(2,2,1,3)))

#use custom latent variable properties (diffuse prior for MAP is very close to ML)
fscores(mod, method='MAP', cov = matrix(1000))
fscores(mod, method='ML')

#WLE estimation, run in parallel using available cores
mirtCluster()
fscores(mod, method='WLE')

#multiple imputation using 30 draws for EAP scores. Requires information matrix
```

```
mod <- mirt(Science, 1, SE=TRUE)
fscores(mod, MI = 30)
```

```
## End(Not run)
```

imputeMissing

Imputing plausible data for missing values

Description

Given an estimated model from any of mirt's model fitting functions and an estimate of the latent trait, impute plausible missing data values. Returns the original data in a `data.frame` without any NA values.

Usage

```
imputeMissing(x, Theta, ...)
```

Arguments

<code>x</code>	an estimated model <code>x</code> from the mirt package
<code>Theta</code>	a matrix containing the estimates of the latent trait scores (e.g., via <code>fscores</code>)
<code>...</code>	additional arguments to pass

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:
dat <- expand.table(LSAT7)
(original <- mirt(dat, 1))
NAperson <- sample(1:nrow(dat), 20, replace = TRUE)
NAitem <- sample(1:ncol(dat), 20, replace = TRUE)
for(i in 1:20)
  dat[NAperson[i], NAitem[i]] <- NA
(mod <- mirt(dat, 1))
scores <- fscores(mod, method = 'MAP', scores.only = TRUE)

#re-estimate imputed dataset (good to do this multiple times and average over)
fulldata <- imputeMissing(mod, scores)
(fullmod <- mirt(fulldata, 1))

#with multipleGroup
group <- rep(c('group1', 'group2'), each=500)
mod2 <- multipleGroup(dat, 1, group)
fs <- fscores(mod2, full.scores=TRUE)
```

```

fullldata2 <- imputeMissing(mod2, fs)

## End(Not run)

```

itemfit

Item fit statistics

Description

itemfit calculates the Z_h values from Drasgow, Levine and Williams (1985), χ^2 values for unidimensional models, and S-X2 statistics for unidimensional models (Kang & Chen, 2007; Orlando & Thissen, 2000). For Rasch, partial credit, and rating scale models infit and outfit statistics are also produced.

Usage

```

itemfit(x, Zh = TRUE, X2 = FALSE, group.size = 150, mincell = 1,
        S_X2.tables = FALSE, empirical.plot = NULL, empirical.CI = 0,
        method = "EAP", Theta = NULL, impute = 0, ...)

```

Arguments

x	a computed model object of class ExploratoryClass, ConfirmatoryClass, or MultipleGroupClass
Zh	logical; calculate Z_h and associated statistics (infit/outfit)? Disable this if you are only interested in computing the S-X2 quickly
X2	logical; calculate the X2 statistic for unidimensional models?
mincell	the minimum expected cell size to be used in the S-X2 computations. Tables will be collapsed across items first if polytomous, and then across scores if necessary
S_X2.tables	logical; return the tables in a list format used to compute the S-X2 stats?
group.size	approximate size of each group to be used in calculating the χ^2 statistic
empirical.plot	a single numeric value or character of the item name indicating which item to plot (via itemplot) and overlay with the empirical θ groupings. Only applicable when type = 'X2'. The default is NULL, therefore no plots are drawn
empirical.CI	a numeric value indicating the width of the empirical confidence interval ranging between 0 and 1 (default of 0 plots not interval). For example, a 95 interval would be plotted if empirical.CI = .95. Only applicable to dichotomous items
method	type of factor score estimation method. See fscores for more detail
Theta	a matrix of factor scores for each person used for statistics that require empirical estimates. If supplied, arguments typically passed to fscores() will be ignored and these values will be used instead. Also required when estimating statistics with missing data via imputation

impute a number indicating how many imputations to perform (passed to `imputeMissing`)
when there are missing data present. This requires a precomputed Theta input.
Will return a data.frame object with the mean estimates of the stats and their
imputed standard deviations

... additional arguments to be passed to `fscores()`

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Drasgow, F., Levine, M. V., & Williams, E. A. (1985). Appropriateness measurement with polychotomous item response models and standardized indices. *Journal of Mathematical and Statistical Psychology*, 38, 67-86.

Kang, T. & Chen, Troy, T. (2007). An investigation of the performance of the generalized S-X2 item-fit index for polytomous IRT models. ACT

Orlando, M. & Thissen, D. (2000). Likelihood-based item fit indices for dichotomous item response theory models. *Applied Psychological Measurement*, 24, 50-64.

Reise, S. P. (1990). A comparison of item- and person-fit methods of assessing model-data fit in IRT. *Applied Psychological Measurement*, 14, 127-137.

Wright B. D. & Masters, G. N. (1982). *Rating scale analysis*. MESA Press.

See Also

[personfit](#)

Examples

```
## Not run:

#make some data
set.seed(1234)
a <- matrix(rlnorm(20, meanlog=0, sdlog = .1), ncol=1)
d <- matrix(rnorm(20), ncol=1)
items <- rep('dich', 20)
data <- simdata(a,d, 2000, items)

x <- mirt(data, 1)
raschfit <- mirt(data, 1, itemtype='Rasch')
fit <- itemfit(x)
fit

itemfit(x, empirical.plot = 1) #empirical item plot
itemfit(x, empirical.plot = 1, empirical.CI = .99) #empirical item plot with 99% CI's
#method='ML' agrees better with eRm package
itemfit(raschfit, method = 'ML') #infit and outfit stats
#same as above, but inputting ML estimates instead
Theta <- fscores(raschfit, method = 'ML', full.scores=TRUE, scores.only=TRUE)
itemfit(raschfit, Theta=Theta)
```

```

#similar example to Kang and Chen 2007
a <- matrix(c(.8,.4,.7, .8, .4, .7, 1, 1, 1, 1))
d <- matrix(rep(c(2.0,0.0,-1,-1.5),10), ncol=4, byrow=TRUE)
dat <- simdata(a,d,2000, itemtype = rep('graded', 10)) - 1
head(dat)

mod <- mirt(dat, 1)
itemfit(mod)

mod2 <- mirt(dat, 1, 'Rasch')
itemfit(mod2)

#massive list of tables
tables <- itemfit(mod, S_X2.tables = TRUE)

#observed and expected total score patterns for item 1 (post collapsing)
tables$O[[1]]
tables$E[[1]]

# fit stats with missing data (run in parallel using all cores)
data[sample(1:prod(dim(data)), 500)] <- NA
raschfit <- mirt(data, 1, itemtype='Rasch')

mirtCluster()
Theta <- fscores(raschfit, method = 'ML', full.scores=TRUE)
itemfit(raschfit, impute = 10, Theta=Theta)

## End(Not run)

```

iteminfo

Function to calculate item information

Description

Given an internal mirt item object extracted by using [extract.item](#), compute the item information.

Usage

```
iteminfo(x, Theta, degrees = NULL, total.info = TRUE)
```

Arguments

x	an extracted internal mirt object containing item information
Theta	a vector (unidimensional) or matrix (multidimensional) of latent trait values
degrees	a vector of angles in degrees that are between 0 and 90 that jointly sum to 90. Only applicable when the input object is multidimensional
total.info	logical; return the total information curve for the item? If FALSE, information curves for each category are returned as a matrix

See Also[extract.item](#)**Examples**

```
## Not run:
mod <- mirt(Science, 1)
extr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-4,4, by = .1))
info.2 <- iteminfo(extr.2, Theta)

#do something with the info?
plot(Theta, info.2, type = 'l', main = 'Item information')

#category information curves
cat.info <- iteminfo(extr.2, Theta, total.info = FALSE)
plot(Theta, cat.info[,1], type = 'l', ylim = c(0, max(cat.info)),
     ylab = 'info', main = 'Category information')
for(i in 2:ncol(cat.info))
  lines(Theta, cat.info[,i], col = i)

## Customized test information plot
T1 <- T2 <- 0
dat <- expand.table(LSAT7)
mod1 <- mirt(dat, 1)
mod2 <- mirt(dat, 1, 'Rasch')
for(i in 1:5){
  T1 <- T1 + iteminfo(extract.item(mod1, i), Theta)
  T2 <- T2 + iteminfo(extract.item(mod2, i), Theta)
}
plot(Theta, T2/T1, type = 'l', ylab = 'Relative Test Information', las = 1)
lines(Theta, T1/T1, col = 'red')

## End(Not run)
```

itemplot

*Displays item surface and information plots***Description**

itemplot displays various item based IRT plots, with special options for plotting items that contain several 0 slope parameters. Supports up to three dimensional models.

Usage

```
itemplot(object, item, type = "trace", degrees = 45, CE = FALSE,
         CEalpha = 0.05, CEdraws = 1000, drop.zeros = FALSE, rot = list(xaxis =
         -70, yaxis = 30, zaxis = 10), theta_lim = c(-6, 6), shiny = FALSE, ...)
```

Arguments

object	a computed model object of class <code>ExploratoryClass</code> , <code>ConfirmatoryClass</code> , or <code>MultipleGroupClass</code> . Input may also be a list for comparing similar item types (e.g., 1PL vs 2PL)
item	a single numeric value, or the item name, indicating which item to plot
type	plot type to use, information ('info'), standard errors ('SE'), item trace lines ('trace'), information and standard errors ('infoSE') or information and trace lines ('infotrace'), relative efficiency lines ('RE'), expected score 'score', or information and trace line contours ('infocontour' and 'tracecontour'); not supported for <code>MultipleGroupClass</code> objects)
degrees	the degrees argument to be used if there are exactly two factors. See <code>iteminfo</code> for more detail
CE	logical; plot confidence envelope?
CEalpha	area remaining in the tail for confidence envelope. Default gives 95% confidence region
CEdraws	draws number of draws to use for confidence envelope
rot	a list of rotation coordinates to be used for 3 dimensional plots
drop.zeros	logical; drop slope values that are numerically close to zero to reduce dimensionality? Useful in objects returned from <code>bfactor</code> or other confirmatory models that contain several zero slopes
theta_lim	lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with <code>npts</code>
shiny	logical; run interactive display for item plots using the shiny interface. This primarily is an instructive tool for demonstrating how item response curves behave when adjusting their parameters
...	additional arguments to be passed to <code>lattice</code> and <code>coef()</code>

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:

data(LSAT7)
fulldata <- expand.table(LSAT7)
mod1 <- mirt(fulldata,1,SE=TRUE)
mod2 <- mirt(fulldata,1, itemtype = 'Rasch')
mod3 <- mirt(fulldata,2)

itemplot(mod1, 2)
itemplot(mod1, 2, CE = TRUE)
itemplot(mod1, 2, type = 'info')
itemplot(mod1, 2, type = 'info', CE = TRUE)
```

```
mods <- list(twoPL = mod1, onePL = mod2)
itemplot(mods, 1, type = 'RE')

#multidimensional
itemplot(mod3, 3, type = 'info')
itemplot(mod3, 3, type = 'infocontour')
itemplot(mod3, 3, type = 'tracecontour')

#polytomous items
pmod <- mirt(Science, 1, SE=TRUE)
itemplot(pmod, 3)
itemplot(pmod, 3, CE = TRUE)
itemplot(pmod, 3, type = 'score')
itemplot(pmod, 3, type = 'infotrace')

# uncomment to run interactive shiny applet
# itemplot(shiny = TRUE)

## End(Not run)
```

key2binary

Convert response patterns to binary data

Description

The key2binary function will convert response pattern data to a dichotomous format, given a response key.

Usage

```
key2binary(fulldata, key)
```

Arguments

fulldata	an object of class data.frame, matrix, or table with the response patterns
key	a vector consisting of the 'correct' response to the items. Each value corresponds to each column in fulldata

Value

Returns a numeric matrix with all the response patterns in dichotomous format.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:
data(SAT12)
head(SAT12)
key <- c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5)

dicho.SAT12 <- key2binary(SAT12,key)

## End(Not run)
```

LSAT6

Description of LSAT6 data

Description

Data from Thissen (1982); contains 5 dichotomously scored items obtained from the Law School Admissions Test, section 6.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Thissen, D. (1982). Marginal maximum likelihood estimation for the one-parameter logistic model. *Psychometrika*, 47, 175-186.

Examples

```
## Not run:
dat <- expand.table(LSAT6)
head(dat)
model <- mirt.model('F = 1-5
                    CONSTRAIN = (1-5, a1)')
(mod <- mirt(dat, model))
coef(mod)

## End(Not run)
```

LSAT7

Description of LSAT7 data

Description

Data from Bock & Lieberman (1970); contains 5 dichotomously scored items obtained from the Law School Admissions Test, section 7.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Bock, R. D., & Lieberman, M. (1970). Fitting a response model for n dichotomously scored items. *Psychometrika*, 35(2), 179-197.

Examples

```
## Not run:
dat <- expand.table(LSAT7)
head(dat)
(mod <- mirt(dat, 1))
coef(mod)

## End(Not run)
```

M2

Compute M2 statistic

Description

Computes the M2 (Maydeu-Olivares & Joe, 2006) statistic for dichotomous data and the M2* statistic for polytomous data (collapsing over response categories for better stability; see Cai and Hansen, 2013), as well as associated fit indices that are based on fitting the null model.

Usage

```
M2(obj, calcNull = TRUE, quadpts = NULL, Theta = NULL, impute = 0,
    CI = 0.9, residmat = FALSE)
```

Arguments

obj	an estimated model object from the mirt package
quadpts	number of quadrature points to use during estimation. If NULL, a suitable value will be chosen based on the rubric found in fscores
calcNull	logical; calculate statistics for the null model as well? Allows for statistics such as the limited information TLI and CFI
Theta	a matrix of factor scores for each person used for imputation
impute	a number indicating how many imputations to perform (passed to imputeMissing) when there are missing data present. This requires a precomputed Theta input. Will return a data.frame object with the mean estimates of the stats and their imputed standard deviations
CI	numeric value from 0 to 1 indicating the range of the confidence interval for RMSEA. Default returns the 90% interval
residmat	logical; return the residual matrix used to compute the SRMSR statistic?

Value

Returns a data.frame object with the M2 statistic, along with the degrees of freedom, p-value, RMSEA (with 90% confidence interval), SRMSR if all items were ordinal, and optionally the TLI and CFI model fit statistics

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Cai, L. & Hansen, M. (2013). Limited-information goodness-of-fit testing of hierarchical item factor models. *British Journal of Mathematical and Statistical Psychology*, 66, 245-276.

Maydeu-Olivares, A. & Joe, H. (2006). Limited information goodness-of-fit testing in multidimensional contingency tables *Psychometrika*, 71, 713-732.

Examples

```
## Not run:
dat <- expand.table(LSAT7)
(mod1 <- mirt(dat, 1))
M2(mod1)

#M2 imputed with missing data present (run in parallel)
dat[sample(1:prod(dim(dat)), 250)] <- NA
mod2 <- mirt(dat, 1)
mirtCluster()
Theta <- fscores(mod2, full.scores=TRUE)
M2(mod2, Theta=Theta, impute = 10)

## End(Not run)
```

mirt	<i>Full-Information Item Factor Analysis (Multidimensional Item Response Theory)</i>
------	--

Description

`mirt` fits an unconditional maximum likelihood factor analysis model to any mixture of dichotomous and polytomous data under the item response theory paradigm using either Cai's (2010) Metropolis-Hastings Robbins-Monro (MHRM) algorithm or with an EM algorithm approach outlined by Bock and Aiken (1981). Models containing 'explanatory' person or item level predictors can only be included by using the `mixedmirt` function. Tests that form a two-tier or bi-factor structure should be estimated with the `bfactor` function, which uses a dimension reduction EM algorithm for modeling item parcels. Multiple group analyses (useful for DIF testing) are also available using the `multipleGroup` function.

Usage

```
mirt(data, model, itemtype = NULL, guess = 0, upper = 1, SE = FALSE,
      SE.type = "crossprod", method = "EM", optimizer = NULL, pars = NULL,
      constrain = NULL, parprior = NULL, calcNull = TRUE, draws = 5000,
      survey.weights = NULL, rotate = "oblimin", Target = NaN,
      quadpts = NULL, TOL = NULL, grsm.block = NULL, key = NULL,
      nominal.highlow = NULL, large = FALSE, GenRandomPars = FALSE,
      accelerate = TRUE, empiricalhist = FALSE, verbose = TRUE,
      technical = list(), ...)
```

Arguments

<code>data</code>	a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
<code>model</code>	an object returned from <code>mirt.model()</code> declaring how the factor model is to be estimated, or a single numeric value indicating the number of exploratory factors to estimate. See <code>mirt.model</code> for more details
<code>itemtype</code>	type of items to be modeled, declared as a vector for each item or a single value which will be repeated globally. The NULL default assumes that the items follow a graded or 2PL structure, however they may be changed to the following: 'Rasch', '2PL', '3PL', '3PLu', '4PL', 'graded', 'grsm', 'gpcm', 'nominal', 'ideal', 'PC2PL', 'PC3PL', '2PLNRM', '3PLNRM', '3PLuNRM', and '4PLNRM', for the Rasch/partial credit, 2 parameter logistic, 3 parameter logistic (lower or upper asymptote upper), 4 parameter logistic, graded response model, rating scale graded response model, generalized partial credit model, nominal model, ideal-point model, 2-3PL partially compensatory model, and 2-4 parameter nested logistic models, respectively. User defined item classes can also be defined using the <code>createItem</code> function
<code>method</code>	a character object specifying the estimation algorithm to be used. The default is 'EM', for the standard EM algorithm with fixed quadrature. The option 'MHRM'

	may also be passed to use the MH-RM algorithm, as well as 'BL' for the Bock and Lieberman approach (generally not recommended for serious use)
optimizer	a character indicating which numerical optimizer to use. By default, the EM algorithm will use the 'BFGS' when there are no upper and lower bounds, and 'L-BFGS-B' when there are. Other options include the Newton-Raphson ('NR'), which often will be more efficient than the 'BFGS' but not as stable for more complex models (such as the nominal or nested logit models) and does not support upper and lower bound constraints. As well, the 'Nelder-Mead' and 'SANN' estimators are also available, but their routine use generally is not required or recommended. The MH-RM algorithm uses the 'NR' by default, and currently cannot be changed
SE	logical; estimate the standard errors by computing the parameter information matrix? See SE.type for the type of estimates available
SE.type	type of estimation method to use for calculating the parameter information matrix for computing standard errors and wald tests. Can be 'MHRM' for stochastic approximation, 'BL' for the Bock and Lieberman approach (numerical evaluation of observed Hessian), 'Fisher' for the expected information, 'complete' for information based on the complete-data Hessian used in EM algorithm (EM only), 'SEM' for the supplemented EM (disables the accelerate option; EM only), 'crossprod' for standard error computations based on the variance of the Fisher scores, 'Louis' for Louis' (1982) computation of the observed information matrix, and 'sandwich' for the sandwich covariance estimate. Note that for 'SEM' option increasing the number of iterations (NCYCLES and TOL, see below) will help to improve the accuracy, and will be run in parallel if a mirtCluster object has been defined. Bootstrapped and profiled-likelihood standard errors are also possible, but must be run with the boot.mirt and PLCI.mirt functions, respectively
guess	fixed pseudo-guessing parameters. Can be entered as a single value to assign a global guessing parameter or may be entered as a numeric vector corresponding to each item
upper	fixed upper bound parameters for 4-PL model. Can be entered as a single value to assign a global guessing parameter or may be entered as a numeric vector corresponding to each item
accelerate	logical; use a general acceleration algorithm described by Ramsey (1975)? Default is TRUE
constrain	a list of user declared equality constraints. To see how to define the parameters correctly use <code>pars = 'values'</code> initially to see how the parameters are labeled. To constrain parameters to be equal create a list with separate concatenated vectors signifying which parameters to constrain. For example, to set parameters 1 and 5 equal, and also set parameters 2, 6, and 10 equal use <code>constrain = list(c(1,5), c(2,6,10))</code> . Constraints can also be specified using the mirt.model syntax (recommended)
parprior	a list of user declared prior item probabilities. To see how to define the parameters correctly use <code>pars = 'values'</code> initially to see how the parameters are labeled. Can define either normal (e.g., intercepts, lower/guessing and upper bounds), log-normal (e.g., for univariate slopes), or beta prior probabilities. To specify a prior the form is <code>c('priortype', ...)</code> , where normal priors are

	<pre>parprior = list(c(parnumbers, 'norm', mean, sd)), parprior = list(c(parnumbers, 'lnorm', for log-normal, and parprior = list(c(parnumbers, 'beta', alpha, beta)) for beta. Priors can also be specified using <code>mirt.model</code> syntax (recommended)</pre>
<code>pars</code>	a data.frame with the structure of how the starting values, parameter numbers, estimation logical values, etc, are defined. The user may observe how the model defines the values by using <code>pars = 'values'</code> , and this object can in turn be modified and input back into the estimation with <code>pars = mymodifiedpars</code>
<code>quadpts</code>	number of quadrature points per dimension (must be larger than 2). By default the number of quadrature uses the following scheme: <code>switch(as.character(nfact), '1'=41, '2'=21</code>
<code>TOL</code>	convergence threshold for EM or MH-RM; defaults are .0001 and .001. If <code>SE.type = 'SEM'</code> and this value is not specified, the default is set to $1e-5$. If <code>empiricalhist = TRUE</code> and <code>TOL</code> is not specified then the default $3e-5$ will be used. To evaluate the model using only the starting values pass <code>TOL = NaN</code>
<code>empiricalhist</code>	logical; estimate prior distribution using an empirical histogram approach. Only applicable for unidimensional models estimated with the EM algorithm. The number of cycles, <code>TOL</code> , and <code>quadpts</code> are adjusted accomodate for less precision during estimation (<code>TOL = 3e-5</code> , <code>NCYCLES = 2000</code> , <code>quadpts = 199</code>)
<code>nominal.highlow</code>	optional matrix indicating the highest (row 1) and lowest (row 2) categories to be used for the nominal response model. Using this input may result in better numerical stability. The matrix input should be a 2 by <code>nitems</code> numeric matrix, where each number represents the <i>reduced</i> category representation (mirt omits categories that are missing, so if the unique values for an item are <code>c(1,2,5,6)</code> they are treated as being the same as <code>c(1,2,3,4)</code> . Viewing the starting values will help to identify the categories)
<code>survey.weights</code>	a optional numeric vector of survey weights to apply for each case in the data (EM estimation only). If not specified, all cases are weighted equally (the standard IRT approach). The sum of the <code>survey.weights</code> must equal the total sample size for proper weighting to be applied
<code>GenRandomPars</code>	logical; generate random starting values prior to optimization instead of using the fixed internal starting values?
<code>grsm.block</code>	an optional numeric vector indicating where the blocking should occur when using the <code>grsm</code> , <code>NA</code> represents items that do not belong to the <code>grsm</code> block (other items that may be estimated in the test data). For example, to specify two blocks of 3 with a 2PL item for the last item: <code>grsm.block = c(rep(1, 3), rep(2, 3), NA)</code> . If <code>NULL</code> the all items are assumed to be within the same group and therefore have the same number of item categories
<code>key</code>	a numeric vector of the response scoring key. Required when using nested logit item types, and must be the same length as the number of items used. Items that are not nested logit will ignore this vector, so use <code>NA</code> in item locations that are not applicable
<code>rotate</code>	type of rotation to perform after the initial orthogonal parameters have been extracted by using <code>summary</code> ; default is <code>'oblimin'</code> . If <code>rotate != ''</code> in the <code>summary</code> input then the default from the object is ignored and the new rotation from the list is used instead. See summary-method for a list of supported rotation options.

Target	a dummy variable matrix indicting a target rotation pattern
calcNull	logical; calculate the Null model for additional fit statistics (e.g., TLI)? Only applicable if the data contains no NA's and the data is not overly sparse
large	either a logical, indicating whether the internal collapsed data should be returned, or a list of internally computed data tables. If TRUE is passed, a list containing the organized tables is returned. This list object can then be passed back into large to avoid reorganizing the data again (useful when the dataset are very large and computing the tabulated data is computationally burdensome). The best strategy for large data is to always pass the internal data to the estimation function, shown below: Compute organized data e.g., <code>internaldat <- mirt(Science, 1, large = TRUE)</code> Pass the organized data to all estimation functions e.g., <code>mod <- mirt(Science, 1, large = internaldat)</code>
draws	the number of Monte Carlo draws to estimate the log-likelihood for the MH-RM algorithm. Default is 5000
verbose	logical; print observed- (EM) or complete-data (MHRM) log-likelihood after each iteration cycle? Default is TRUE
technical	a list containing lower level technical parameters for estimation. May be: MAXQUAD maximum number of quadratures, which you can increase if you have more than 4GB or RAM on your PC; default 10000 NCYCLES maximum number of EM or MH-RM cycles; defaults are 500 and 2000 BURNIN number of burn in cycles (stage 1) in MH-RM; default 150 SEMCYCLES number of SEM cycles (stage 2) in MH-RM; default 50 set.seed seed number used during estimation. Default is 12345 symmetric_SEM logical; force S-EM information matrix to be symmetric? Default is TRUE so that computation of standard errors are more stable. Setting this to FALSE can help to detect solutions that have not reached the ML estimate gain a vector of two values specifying the numerator and exponent values for the RM gain function $(val1/cycle)^{val2}$. Default is <code>c(0.15, 0.65)</code> warn logical; include warning messages during estimation? Default is TRUE message logical; include general messages during estimation? Default is TRUE customK a numeric vector used to explicitly declare the number of response categories for each item. This should only be used when constructing mirt model for reasons other than parameter estimation (such as to obtain factor scores), and requires that the input data all have 0 as the lowest category. The format is the same as the <code>mod@K</code> slot in all converged models customPriorFun a custom function used to determine the normalized density for integration in the EM algorithm. Must be of the form <code>function(Theta, Etable){...}</code> , and return a numeric vector with the same length as number of rows in Theta. The Etable input contains the aggregated table generated from the current E-step computations. For proper integration, the returned vector should sum to 1 (i.e., normalized). Note that if using the Etable it will be NULL on the first call, therefore the prior will have to deal with this issue accordingly

customTheta a custom Theta grid, in matrix form, used for integration. If not defined, the grid is determined internally based on the number of quadpts

MHcand a vector of values used to tune the MH sampler. Larger values will cause the acceptance ratio to decrease. One value is required for each group in unconditional item factor analysis (`mixedmirt()` requires additional values for random effect). If null, these values are determined internally, attempting to tune the acceptance of the draws to be between .1 and .4

parallel logical; use the parallel cluster defined by `mirtCluster`? Default is TRUE

... additional arguments to be passed

Value

function returns an object of class `ExploratoryClass` ([ExploratoryClass-class](#)) if the estimated model was exploratory, or `ConfirmatoryClass` ([ConfirmatoryClass-class](#)) if the model has unique axes that do not require rotation.

Confirmatory and Exploratory IRT

Specification of the confirmatory item factor analysis model follows many of the rules in the structural equation modeling framework for confirmatory factor analysis. The variances of the latent factors are automatically fixed to 1 to help facilitate model identification. All parameters may be fixed to constant values or set equal to other parameters using the appropriate declarations. If the model is confirmatory then the returned class will be a 'ConfirmatoryClass'. Confirmatory models may also contain 'explanatory' person or item level predictors, though including predictors is currently limited to the `mixedmirt` function.

When specifying a single number greater than 1 as the `model` input to `mirt` an exploratory IRT model will be estimated. Rotation and target matrix options will be used in this subroutine and will be passed to the returned object for use in generic functions such as `summary()` and `fscores()`. Again, factor means and variances are fixed to ensure proper identification. If the model is exploratory then the returned class will be 'ExploratoryClass', otherwise it will be of class 'ConfirmatoryClass'.

If the model is an exploratory item factor analysis estimation will begin by computing a matrix of quasi-polychoric correlations. A factor analysis with `nfact` is then extracted and item parameters are estimated by $a_{ij} = f_{ij}/u_j$, where f_{ij} is the factor loading for the j th item on the i th factor, and u_j is the square root of the factor uniqueness, $\sqrt{1 - h_j^2}$. The initial intercept parameters are determined by calculating the inverse normal of the item facility (i.e., item easiness), q_j , to obtain $d_j = q_j/u_j$. A similar implementation is also used for obtaining initial values for polytomous items.

A note on upper and lower bound parameters

Internally the g and u parameters are transformed using a logit transformation ($\log(x/(1-x))$), and can be reversed by using $1/(1 + \exp(-x))$ following convergence. This also applies when computing confidence intervals for these parameters, and is done so automatically if `coef(mod, rawug = FALSE)`.

As such, when applying prior distributions to these parameters it is recommended to use a prior that ranges from negative infinity to positive infinity, such as the normally distributed prior via the 'norm' input (see `mirt.model`).

Convergence for quadrature methods

Unrestricted full-information factor analysis is known to have problems with convergence, and some items may need to be constrained or removed entirely to allow for an acceptable solution. As a general rule dichotomous items with means greater than .95, or items that are only .05 greater than the guessing parameter, should be considered for removal from the analysis or treated with prior parameter distributions. The same type of reasoning is applicable when including upper bound parameters as well. For polytomous items, if categories are rarely endorsed then this will cause similar issues. Also, increasing the number of quadrature points per dimension may help to stabilize the estimation process in higher dimensions. Finally, solutions that are not well defined also will have difficulty converging, and can indicate that the model has been misspecified (e.g., extracting too many dimensions).

Convergence for MH-RM method

For the MH-RM algorithm, when the number of iterations grows very high (e.g., greater than 1500) or when `Max Change = .2500` values are repeatedly printed to the console too often (indicating that the parameters were being constrained since they are naturally moving in steps greater than 0.25) then the model may either be ill defined or have a very flat likelihood surface, and genuine maximum-likelihood parameter estimates may be difficult to find. Standard errors are computed following the model convergence by passing `SE = TRUE`, to perform an additional MH-RM stage but treating the maximum-likelihood estimates as fixed points.

Additional helper functions

Additional functions are available in the package which can be useful pre- and post-estimation. These are:

- `mirt.model` Define the IRT model specification use special syntax. Useful for defining between and within group parameter constraints, prior parameter distributions, and specifying the slope coefficients for each factor
- `coef-method` Extract raw coefficients from the model, along with their standard errors and confidence intervals
- `summary-method` Extract standardized loadings from model. Accepts a `rotate` argument for exploratory item response model
- `anova-method` Compare nested models using likelihood ratio statistics as well as information criteria such as the AIC and BIC
- `residuals-method` Compute pairwise residuals between each item using methods such as the LD statistic (Chen & Thissen, 1997), as well as response pattern residuals
- `plot-method` Plot various types of test level plots including the test score and information functions and more
- `itemplot` Plot various types of item level plots, including the score, standard error, and information functions, and more
- `createItem` Create a customized `itemtype` that does not currently exist in the package
- `imputeMissing` Impute missing data given some computed Theta matrix
- `fscores` Find predicted scores for the latent traits using estimation methods such as EAP, MAP, ML, WLE, and EAPsum

- wald** Compute Wald statistics follow the convergence of a model with a suitable information matrix
- M2** Limited information goodness of fit test statistic based to determine how well the model fits the data
- itemfit and personfit** Goodness of fit statistics at the item and person levels, such as the S-X2, infit, outfit, and more
- boot.mirt and PLCI.mirt** Compute estimated parameter confidence intervals via the bootstrap and profiled-likelihood methods
- read.mirt** Translates mirt objects into objects suitable for use with the plink package
- mirtCluster** Define a cluster for the package functions to use for capitalizing on multi-core architecture to utilize available CPUs when possible. Will help to decrease estimation times for tasks that can be run in parallel

IRT Models

The parameter labels use the follow convention, here using two factors and k as the number of categories.

Rasch Only one intercept estimated, and the latent variance of θ is freely estimated. If the data have more than two categories then a partial credit model is used instead (see 'gpcm' below).

$$P(x = 1|\theta, d) = \frac{1}{1 + \exp(-(\theta + d))}$$

2-4PL Depending on the model u may be equal to 1 and g may be equal to 0.

$$P(x = 1|\theta, \psi) = g + \frac{(u - g)}{1 + \exp(-(a_1 * \theta_1 + a_2 * \theta_2 + d))}$$

graded The graded model consists of sequential 2PL models, and here k is the predicted category.

$$P(x = k|\theta, \psi) = P(x \geq k|\theta, \phi) - P(x \geq k + 1|\theta, \phi)$$

grsm A more constrained version of the graded model where graded spacing is equal across item blocks and only adjusted by a single 'difficulty' parameter (c) while the latent variance of θ is freely estimated. Again,

$$P(x = k|\theta, \psi) = P(x \geq k|\theta, \phi) - P(x \geq k + 1|\theta, \phi)$$

but now

$$P = \frac{1}{1 + \exp(-(a_1 * \theta_1 + a_2 * \theta_2 + d_k + c))}$$

gpcm/nominal For the gpcm the d values are treated as fixed and ordered values from 0:(k-1) (in the nominal model d_0 is also set to 0). Additionally, for identification in the nominal model $ak_0 = 0, ak_{(k-1)} = (k - 1)$.

$$P(x = k|\theta, \psi) = \frac{\exp(ak_{k-1} * (a_1 * \theta_1 + a_2 * \theta_2) + d_{k-1})}{\sum_1^k \exp(ak_{k-1} * (a_1 * \theta_1 + a_2 * \theta_2) + d_{k-1})}$$

For partial credit model (when `itemtype = 'Rasch'`; unidimensional only) the above model is further constrained so that $ak = (0, 1, \dots, k - 1)$, $a_1 = 1$, and the latent variance of θ_1 is freely estimated.

In the nominal model this parametrization helps to identify the empirical ordering of the categories by inspecting the ak values. Larger values indicate that the item category is more positively related to the latent trait(s) being measured. For instance, if an item was truly ordinal (such as a Likert scale), and had 4 response categories, we would expect to see $ak_0 < ak_1 < ak_2 < ak_3$ following estimation. If on the other hand $ak_0 > ak_1$ then it would appear that the second category is less related to the trait than the first, and therefore the second category should be understood as the 'lowest score'.

NOTE: The nominal model can become numerical unstable if poor choices for the high and low values are chosen, resulting in ak values greater than $\text{abs}(10)$ or more. It is recommended to choose high and low anchors that cause the estimated parameters to fall between 0 and the number of categories - 1 either by theoretical means or by re-estimating the model with better values following convergence.

ideal The ideal point model has the form, with the upper bound constraint on d set to 0:

$$P(x = 1|\theta, \psi) = \exp(-0.5 * (a_1 * \theta_1 + a_2 * \theta_2 + d)^2)$$

partcomp Partially compensatory models consist of the product of 2PL probability curves.

$$P(x = 1|\theta, \psi) = g + (1 - g) \left(\frac{1}{1 + \exp(-(a_1 * \theta_1 + d_1))} * \frac{1}{1 + \exp(-(a_2 * \theta_2 + d_2))} \right)$$

2-4PLNRM Nested logistic curves for modeling distractor items. Requires a scoring key. The model is broken into two components for the probability of endorsement. For successful endorsement the probability trace is the 1-4PL model, while for unsuccessful endorsement:

$$P(x = 0|\theta, \psi) = (1 - P_{1-4PL}(x = 1|\theta, \psi)) * P_{nominal}(x = k|\theta, \psi)$$

which is the product of the compliment of the dichotomous trace line with the nominal response model. In the nominal model, the slope parameters defined above are constrained to be 1's, while the last value of the ak is freely estimated.

HTML help files, exercises, and examples

To access examples, vignettes, and exercise files that have been generated with knitr please visit <http://philchalmers.github.io/mirt/mirt-vignettes.html>.

Author(s)

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See Also

[bfactor](#), [multipleGroup](#), [mixedmirt](#), [expand.table](#), [key2binary](#), [mod2values](#), [extract.item](#), [iteminfo](#), [testinfo](#), [probtrace](#), [simdata](#)

Examples

```
## Not run:
#load LSAT section 7 data and compute 1 and 2 factor models
data <- expand.table(LSAT7)

(mod1 <- mirt(data, 1))
coef(mod1)
(mod2 <- mirt(data, 1, SE = TRUE)) #standard errors with crossprod method
(mod2 <- mirt(data, 1, SE = TRUE, SE.type = 'SEM')) #standard errors with SEM method
coef(mod2)
(mod3 <- mirt(data, 1, SE = TRUE, SE.type = 'BL')) #standard errors with BL method
residuals(mod1)
plot(mod1) #test information function
plot(mod1, type = 'trace') #trace lines
plot(mod2, type = 'score') #expected total score
plot(mod2, type = 'score', MI=200) #expected total score with 95% confidence intervals

#estimated 3PL model for item 5 only
(mod1.3PL <- mirt(data, 1, itemtype = c('2PL', '2PL', '2PL', '2PL', '3PL')))
coef(mod1.3PL)
#internally g and u pars are stored as logits, so usually a good idea to include normal prior
# to help stabilize the parameters. For a value around .182 use a mean
# of -1.5 (since 1 / (1 + exp(-(-1.5))) == .182)
(mod1.3PL.norm <- mirt(data, 1, itemtype = c('2PL', '2PL', '2PL', '2PL', '3PL'),
  parprior = list(c(19, 'norm', -1.5, 3))))
coef(mod1.3PL.norm)

#could also define priors using mirt.model() syntax
model <- mirt.model('F = 1-5
  PRIOR = (5, g, norm, -1.5, 3)')
mod1.3PL.norm2 <- mirt(data, model, itemtype = c('2PL', '2PL', '2PL', '2PL', '3PL'))
coef(mod1.3PL.norm2)
#limited information fit statistics
M2(mod1.3PL.norm)

#unidimensional ideal point model
idealpt <- mirt(data, 1, itemtype = 'ideal')
plot(idealpt, type = 'trace', facet_items = TRUE)
plot(idealpt, type = 'trace', facet_items = FALSE)

#two factors (exploratory)
mod2 <- mirt(data, 2)
coef(mod2)
summary(mod2, rotate = 'oblimin') #oblimin rotation
residuals(mod2)
plot(mod2)

anova(mod1, mod2) #compare the two models
scores <- fscores(mod2) #save factor score table
scoresfull <- fscores(mod2, full.scores = TRUE, scores.only = TRUE) #factor scores

#confirmatory (as an example, model is not identified since you need 3 items per factor)
```



```

cmodel <- mirt.model('
  F1 = 1,4,5
  F2 = 2,3')

cmod <- mirt(data, cmodel)
coef(cmod)
anova(cmod, mod2)
#check if identified by computing information matrix
(cmod <- mirt(data, cmodel, SE = TRUE))

#####
#data from the 'ltm' package in numeric format
pmod1 <- mirt(Science, 1)
plot(pmod1)
summary(pmod1)

#Constrain all slopes to be equal with the constrain = list() input or mirt.model() syntax
#first obtain parameter index
values <- mirt(Science,1, pars = 'values')
values #note that slopes are numbered 1,5,9,13, or index with values$parnum[values$name == 'a1']
(pmod1_equalslopes <- mirt(Science, 1, constrain = list(c(1,5,9,13))))
coef(pmod1_equalslopes)

# using mirt.model syntax, constrain all item slopes to be equal
model <- mirt.model('
  F = 1-4
  CONSTRAIN = (1-4, a1)')
(pmod1_equalslopes <- mirt(Science, model))
coef(pmod1_equalslopes)

coef(pmod1_equalslopes)
anova(pmod1_equalslopes, pmod1) #significantly worse fit with almost all criteria

pmod2 <- mirt(Science, 2)
summary(pmod2)
plot(pmod2)
itemplot(pmod2, 1)
anova(pmod1, pmod2)

#unidimensional fit with a generalized partial credit and nominal model
(gpcmod <- mirt(Science, 1, 'gpcm'))
coef(gpcmod)

#for the nominal model the lowest and highest categories are assumed to be the
# theoretically lowest and highest categories that related to the latent trait(s), however
# a custom nominal.highlow matrix can be passed to declare which item category should be
# treated as the 'highest' and 'lowest' instead
(nomod <- mirt(Science, 1, 'nominal'))
coef(nomod) #ordering of ak values suggest that the items are indeed ordinal
anova(gpcmod, nomod)
itemplot(nomod, 3)

## example applying survey weights.

```

```

# weight the first half of the cases to be more representative of population
survey.weights <- c(rep(2, nrow(Science)/2), rep(1, nrow(Science)/2))
survey.weights <- survey.weights/sum(survey.weights) * nrow(Science)
unweighted <- mirt(Science, 1)
weighted <- mirt(Science, 1, survey.weights=survey.weights)

#####
#empirical dimensionality testing that includes 'guessing'

data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

mod1 <- mirt(data, 1)
slot(mod1, 'time') #time elapsed for each estimation component

#optionally use Newton-Raphson for (generally) faster convergence in the M-step's
mod1 <- mirt(data, 1, optimizer = 'NR')
slot(mod1, 'time')

mod2 <- mirt(data, 2, optimizer = 'NR')
#difficulty converging with reduced quadpts, reduce TOL
mod3 <- mirt(data, 3, TOL = .001, optimizer = 'NR')
anova(mod1,mod2)
anova(mod2, mod3) #negative AIC, 2 factors probably best

#with fixed guessing parameters
mod1g <- mirt(data, 1, guess = .1)
coef(mod1g)

#####
#graded rating scale example

#make some data
set.seed(1234)
a <- matrix(rep(1, 10))
d <- matrix(c(1,0.5,-.5,-1), 10, 4, byrow = TRUE)
c <- seq(-1, 1, length.out=10)
data <- simdata(a, d + c, 2000, itemtype = rep('graded',10))

mod1 <- mirt(data, 1)
mod2 <- mirt(data, 1, itemtype = 'grsm')
coef(mod2)
anova(mod2, mod1) #not sig, mod2 should be preferred
itemplot(mod2, 1)
itemplot(mod2, 5)
itemplot(mod2, 10)

#####
# 2PL nominal response model example (Suh and Bolt, 2010)
data(SAT12)
SAT12[SAT12 == 8] <- NA
head(SAT12)

```

```

#correct answer key
key <- c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5)
scoredSAT12 <- key2binary(SAT12, key)
mod0 <- mirt(scoredSAT12, 1)

#for first 5 items use 2PLNRM and nominal
scoredSAT12[,1:5] <- as.matrix(SAT12[,1:5])
mod1 <- mirt(scoredSAT12, 1, c(rep('nominal',5),rep('2PL', 27)))
mod2 <- mirt(scoredSAT12, 1, c(rep('2PLNRM',5),rep('2PL', 27)), key=key)
coef(mod0)$Item.1
coef(mod1)$Item.1
coef(mod2)$Item.1
itemplot(mod0, 1)
itemplot(mod1, 1)
itemplot(mod2, 1)

#compare added information from distractors
Theta <- matrix(seq(-4,4,.01))
par(mfrow = c(2,3))
for(i in 1:5){
  info <- iteminfo(extract.item(mod0,i), Theta)
  info2 <- iteminfo(extract.item(mod2,i), Theta)
  plot(Theta, info2, type = 'l', main = paste('Information for item', i), ylab = 'Information')
  lines(Theta, info, col = 'red')
}
par(mfrow = c(1,1))

#test information
plot(Theta, testinfo(mod2, Theta), type = 'l', main = 'Test information', ylab = 'Information')
lines(Theta, testinfo(mod0, Theta), col = 'red')

#####
# using the MH-RM algorithm
data(LSAT7)
fulldata <- expand.table(LSAT7)
(mod1 <- mirt(fulldata, 1, method = 'MHRM'))

#Confirmatory models

#simulate data
a <- matrix(c(
1.5,NA,
0.5,NA,
1.0,NA,
1.0,0.5,
NA,1.5,
NA,0.5,
NA,1.0,
NA,1.0),ncol=2,byrow=TRUE)

d <- matrix(c(
-1.0,NA,NA,

```

```

-1.5,NA,NA,
 1.5,NA,NA,
 0.0,NA,NA,
 3.0,2.0,-0.5,
 2.5,1.0,-1,
 2.0,0.0,NA,
 1.0,NA,NA),ncol=3,byrow=TRUE)

sigma <- diag(2)
sigma[1,2] <- sigma[2,1] <- .4
items <- c(rep('dich',4), rep('graded',3), 'dich')
dataset <- simdata(a,d,2000,items,sigma)

#analyses
#CIFA for 2 factor crossed structure

model.1 <- mirt.model('
  F1 = 1-4
  F2 = 4-8
  COV = F1*F2')

#compute model, and use parallel computation of the log-likelihood
mirtCluster()
mod1 <- mirt(dataset, model.1, method = 'MHRM')
coef(mod1)
summary(mod1)
residuals(mod1)

#####
#bifactor
model.3 <- mirt.model('
  G = 1-8
  F1 = 1-4
  F2 = 5-8')

mod3 <- mirt(dataset,model.3, method = 'MHRM')
coef(mod3)
summary(mod3)
residuals(mod3)
anova(mod1,mod3)

#####
#polynomial/combinations
data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

model.quad <- mirt.model('
  F1 = 1-32
  (F1*F1) = 1-32')

model.combo <- mirt.model('

```

```

      F1 = 1-16
      F2 = 17-32
      (F1*F2) = 1-8')

(mod.quad <- mirt(data, model.quad))
(mod.combo <- mirt(data, model.combo))
anova(mod.quad, mod.combo)

#non-linear item and test plots
plot(mod.quad)
plot(mod.combo, type = 'SE')
itemplot(mod.quad, 1, type = 'score')
itemplot(mod.combo, 2, type = 'score')
itemplot(mod.combo, 2, type = 'infocontour')

## empical histogram examples (normal, skew and bimodality)
#make some data
set.seed(1234)
a <- matrix(rlnorm(50, .2, .2))
d <- matrix(rnorm(50))
ThetaNormal <- matrix(rnorm(2000))
ThetaBimodal <- scale(matrix(c(rnorm(1000, -2), rnorm(1000,2)))) #bimodal
ThetaSkew <- scale(matrix(rchisq(2000, 3))) #positive skew
datNormal <- simdata(a, d, 2000, itemtype = 'dich', Theta=ThetaNormal)
datBimodal <- simdata(a, d, 2000, itemtype = 'dich', Theta=ThetaBimodal)
datSkew <- simdata(a, d, 2000, itemtype = 'dich', Theta=ThetaSkew)

normal <- mirt(datNormal, 1, empiricalhist = TRUE)
plot(normal, type = 'empiricalhist')
histogram(ThetaNormal, breaks=30)

bimodal <- mirt(datBimodal, 1, empiricalhist = TRUE)
plot(bimodal, type = 'empiricalhist')
histogram(ThetaBimodal, breaks=30)

skew <- mirt(datSkew, 1, empiricalhist = TRUE)
plot(skew, type = 'empiricalhist')
histogram(ThetaSkew, breaks=30)

## End(Not run)

```

mirt.model

Specify model loadings

Description

The `mirt.model` function scans/reads user input to specify the confirmatory model.

Usage

```
mirt.model(input = NULL, file = "", COV = NULL, quiet = TRUE, ...)
```

Arguments

input	input for writing out the model syntax. Can either be a string declaration of class character or the so-called Q-matrix or class matrix that specifies the model either with integer or logical values. If the Q-matrix method is chosen covariances terms can be specified with the COV input
file	a input specifying an external file that declares the input.
COV	a symmetric, logical matrix used to declare which covariance terms are estimated
quiet	logical argument passed to scan() to suppress console read message
...	additional arguments for scan()

Details

Factors are first named and then specify which numerical items they affect (i.e., where the slope is not equal to 0), separated either by commas or by - to indicate a range of items. Products between factors may be specified by enclosing the left hand term within brackets. To finish the declaration of a model simply enter a blank line with only a carriage return (i.e., the 'enter' or 'return' key), or instead read in an input version of the model syntax.

There is an optional keyword for specifying the correlation between relationships between factors called COV, and non-linear factor products can be included by enclosing the product combination on the left hand side of the declaration (e.g., (F1*F1) would create a quadratic factor for F1).

COV Specify the relationship between the latent factors. Estimating a correlation between factors is declared by joining the two factors with an asterisk (e.g., F1*F2), or with an asterisk between three or more factors to estimate all the possible correlations (e.g., F1*F2*F3)

CONSTRAIN A bracketed, comma separated list specifying equality constrains between items.

The input format is `CONSTRAIN = (items, ..., parameterName, OptionalGroup), (items, ..., parameterName)`

If `OptionalGroup` is omitted then the constraints are applied within all groups. For example, in a single group 10-item dichotomous tests, using the default 2PL model, the first and last 5 item slopes (a1) can be constrained to be equal by using `CONSTRAIN = (1-5, a1), (6-10, a1)`, or some combination such as `CONSTRAIN = (1-3,4,5,a1), (6,7,8-10,a1)`

CONSTRAINB A bracketed, comma separate list specifying equality constrains between groups.

The input format is `CONSTRAINB = (items, ..., parameterName), (items, ..., parameterName)`.

For example, in a two group 10-item dichotomous tests, using the default 2PL model, the first 5 item slopes (a1) can be constrained to be equal across both groups by using `CONSTRAINB = (1-5, a1)`, or some combination such as `CONSTRAINB = (1-3,4,5,a1)`

PRIOR A bracketed, comma separate list specifying prior parameter distributions. The input format is `PRIOR = (items, ..., parameterName, priorType, val1, val2, OptionalGroup), (items, ..., parameterName)`

If `OptionalGroup` is omitted then the priors are defined for all groups. For example, in a single group 10-item dichotomous tests, using the default 2PL model, defining a normal prior of $N(0,2)$ for the first 5 item intercepts (d) can be defined by `PRIOR = (1-5, d, norm, 0, 2)`

MEAN A comma separated list specifying which latent factor means to freely estimate. E.g.,

`MEAN = F1, F2` will free the latent means for factors F1 and F2

Value

Returns a model specification object to be used in `mirt`, `bfactor`, `multipleGroup`, or `mixedmirt`

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:

model <- mirt.model()
  F1 = 1,2,3,4-10
  F2 = 10-20
  (F1*F2) = 1,2,3,4-10
  COV = F1*F2

#Or alternatively
s <- 'F1 = 1,2,3,4-10
     F2 = 10-20
     (F1*F2) = 1,2,3,4-10
     COV = F1*F2'
model <- mirt.model(s)

#Q-matrix specification
Q <- matrix(c(1,1,1,0,0,0,0,0,0,0,1,1,1), ncol=2, dimnames = list(NULL, c('Factor1', 'Factor2')))
COV <- matrix(c(FALSE, TRUE, TRUE, FALSE), 2)
model <- mirt.model(Q, COV=COV)

## constrain various items slopes and all intercepts in single group model to be equal,
# and use a log-normal prior for all the slopes
s <- 'F = 1-10
     CONSTRAIN = (1-3, 5, 6, a1), (1-10, d)
     PRIOR = (1-10, a1, lnorm, .2, .2)'
model <- mirt.model(s)

## constrain various items slopes and intercepts across groups for use in multipleGroup(),
# and constrain first two slopes within 'group1' to be equal
s <- 'F = 1-10
     CONSTRAIN = (1-2, a1)
     CONSTRAINB = (1-3, 5, 6, a1), (1-10, d)'
model <- mirt.model(s)

## End(Not run)
```

`mirtCluster`*Define a parallel cluster object to be used in internal functions*

Description

This function defines an object that is placed in a relevant internal environment defined in `mirt`. Internal functions such as `calcLogLik`, `fscores`, etc, will utilize this object automatically to capitalize on parallel processing architecture. The object defined is a call from `parallel::makeCluster()`. Note that if you are defining other parallel objects (for simulation designs, for example) it is not recommended to define a `mirtCluster`.

Usage

```
mirtCluster(ncores, remove = FALSE)
```

Arguments

<code>ncores</code>	number of cores to be used in the returned object which is passed to <code>parallel::makeCluster()</code> . If no input is given the maximum number of available cores will be used
<code>remove</code>	logical; remove previously defined <code>mirtCluster()</code> ?

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:  
  
#make 4 cores available for parallel computing  
mirtCluster(4)  
  
#' #stop and remove cores  
mirtCluster(remove = TRUE)  
  
#use all available cores  
mirtCluster()  
  
## End(Not run)
```

MixedClass-class	<i>Class "MixedClass"</i>
------------------	---------------------------

Description

Defines the object returned from `mixedmirt`.

Slots

Data: Object of class "list", contains various data matrices and properties
iter: Object of class "numeric", number of iterations
pars: Object of class "list", estimated parameter objects list
shortpars: Object of class "numeric", unique estimated parameters
model: Object of class "list", list containing original model
K: Object of class "numeric", number of item categories
itemloc: Object of class "numeric", index for tabdata
df: Object of class "numeric", degrees of freedom
AIC: Object of class "numeric", Akaike's information criteria
BIC: Object of class "numeric", Bayesian information criteria
G2: Object of class "numeric", G squared stat
p: Object of class "numeric", p-value for G2
df: Object of class "numeric", degrees of freedom
RMSEA: Object of class "numeric", root mean-square error of approximation for G2
TLI: Object of class "numeric", Tucker-Lewis index for G2
CFI: Object of class "numeric", CFI for G2
logLik: Object of class "numeric", observed log-likelihood
SElogLik: Object of class "numeric", Monte Carlo standard error for log-likelihood
F: Object of class "matrix", unrotated factor loadings
h2: Object of class "numeric", commonalities
Theta: Object of class "matrix", ability grid
Pl: Object of class "numeric", normed likelihoods for tabulated response
prodlist: Object of class "list", list containing product combination of factors
converge: Object of class "numeric", convergence diagnostic
quadpts: Object of class "numeric", number of quadrature points
eststype: Object of class "character", indicates whether estimation was 'EM' or 'MHRM'
cand.t.var: Object of class "numeric", parameter used to control the MH sampler for Theta
random: Object of class "list", typically null, except for internal mixed model usage
null.mod: Object of class "ExploratoryClass", null model

condnum: Object of class "numeric", condition number of information matrix
secondordertest: Object of class "logical", indicate whether information matrix passes second-order test
infomethod: Object of class "character", indicates which information estimation method was used
TOL: Object of class "numeric", tolerance stopping criteria
CUSTOM.IND: Object of class "integer", an internal index
SLOW.IND: Object of class "integer", an internal index
Call: Object of class "call", call

Methods

coef signature(object = "MixedClass")
print signature(x = "MixedClass")
residuals signature(object = "MixedClass")
show signature(object = "MixedClass")
summary signature(object = "MixedClass")
logLik signature(object = "MixedClass")
anova signature(object = "MixedClass")

Author(s)

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mixedmirt

Mixed effects modeling for MIRT models

Description

mixedmirt fits MIRT models using FIML estimation to dichotomous and polytomous IRT models conditional on fixed and random effect of person and item level covariates. This can also be understood as 'explanatory IRT' if only fixed effects are modeled, or multilevel/mixed IRT if random and fixed effects are included. The method uses the MH-RM algorithm exclusively. Additionally, computation of the log-likelihood can be sped up by using parallel estimation via [mirtCluster](#).

Usage

```

mixedmirt(data, covdata = NULL, model, fixed = ~1, random = NULL,
  itemtype = "Rasch", itemdesign = NULL, constrain = NULL, pars = NULL,
  return.design = FALSE, SE = TRUE, ...)
  
```

Arguments

data	a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
covdata	a data.frame that consists of the nrow(data) by K 'person level' fixed and random predictors
model	an object returned from <code>mirt.model()</code> declaring how the factor model is to be estimated. See <code>mirt.model</code> for more details
fixed	a right sided R formula for specifying the fixed effect (aka 'explanatory') predictors from covdata and itemdesign. To estimate the intercepts for each item the keyword <code>items</code> is reserved and automatically added to the <code>itemdesign</code> input. If any polytomous items are being model the <code>items</code> are argument is not valid since all intercept parameters are freely estimated and identified with the parameterizations found in <code>mirt</code> , and the first column in the fixed design matrix (commonly the intercept or a reference group) is omitted
random	a right sided formula or list of formulas containing crossed random effects of the form <code>v1 + ... v_n G</code> , where G is the grouping variable and v_n are random numeric predictors within each group. If no intercept value is specified then by default the correlations between the v's and G are estimated, but can be suppressed by including the <code>~ -1 + ... constant</code>
itemtype	same as <code>itemtype</code> in <code>mirt</code> , expect does not support the following item types: <code>c('PC2PL', 'PC3PL', '2PLNRM', '3PLNRM', '3PLuNRM', '4PLNRM')</code>
itemdesign	a data.frame object used to create a design matrix for the items, where each <code>nrow(itemdesign) == nitems</code> and the number of columns is equal to the number of fixed effect predictors (i.e., item intercepts). By default an <code>items</code> variable is reserved for modeling the item intercept parameters
constrain	a list indicating parameter equality constrains. See <code>mirt</code> for more detail
pars	used for parameter starting values. See <code>mirt</code> for more detail
return.design	logical; return the design matrices before they have (potentially) been reassigned?
SE	logical; compute the standard errors by approximating the information matrix using the MHRM algorithm? Default is TRUE
...	additional arguments to be passed to the MH-RM estimation engine. See <code>mirt</code> for more details and examples

Details

For dichotomous response models, `mixedmirt` follows the general form

$$P(x = 1|\theta, \psi) = g + \frac{(u - g)}{1 + \exp(-1 * [\theta\mathbf{a} + \mathbf{X}\beta + \mathbf{Z}\delta])}$$

where X is a design matrix with associated β fixed effect coefficients, and Z is a design matrix with associated δ random effects. For simplicity and easier interpretation, the unique item intercept values typically found in $\mathbf{X}\beta$ are extracted and reassigned within `mirt`'s 'intercept' parameters (e.g.,

'd'). To observe how the design matrices are structured prior to reassignment and estimation pass the argument `return.design = TRUE`.

Polytomous IRT models follow a similar format except the item intercepts are automatically estimated internally, rendering the `items` argument in the fixed formula redundant and therefore must be omitted from the specification. If there are a mixture of dichotomous and polytomous items the intercepts for the dichotomous models are also estimated for consistency.

To simulate maximum a posteriori estimates for the random effects use the [randef](#) function.

Value

function returns an object of class `MixedClass` ([MixedClass-class](#)).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

See Also

[mirt](#), [randef](#)

Examples

```
## Not run:

#make some data
set.seed(1234)
N <- 750
a <- matrix(rlnorm(10,.3,1),10,1)
d <- matrix(rnorm(10), 10)
Theta <- matrix(sort(rnorm(N)))
pseudoIQ <- Theta * 5 + 100 + rnorm(N, 0 , 5)
pseudoIQ <- (pseudoIQ - mean(pseudoIQ))/10 #rescale variable for numerical stability
group <- factor(rep(c('G1','G2','G3'), each = N/3))
data <- simdata(a,d,N, itemtype = rep('dich',10), Theta=Theta)
covdata <- data.frame(group, pseudoIQ)
#use parallel computing
mirtCluster()

#specify IRT model
model <- mirt.model('Theta = 1-10')

#model with no person predictors
mod0 <- mirt(data, model, itemtype = 'Rasch')

#group as a fixed effect predictor (aka, uniform dif)
mod1 <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items)
anova(mod0, mod1)
summary(mod1)
coef(mod1)

#same model as above in lme4
```

```

wide <- data.frame(id=1:nrow(data),data,covdata)
long <- reshape2::melt(wide, id.vars = c('id', 'group', 'pseudoIQ'))
library(lme4)
lmod0 <- glmer(value ~ 0 + variable + (1|id), long, family = binomial)
lmod1 <- glmer(value ~ 0 + group + variable + (1|id), long, family = binomial)
anova(lmod0, lmod1)

#model using 2PL items instead of Rasch
mod1b <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items, itemtype = '2PL')
anova(mod1, mod1b) #better with 2PL models using all criteria (as expected, given simdata pars)

#continuous predictor with group
mod2 <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items + pseudoIQ)
summary(mod2)
anova(mod1b, mod2)

#view fixed design matrix with and without unique item level intercepts
withint <- mixedmirt(data, covdata, model, fixed = ~ 0 + items + group, return.design = TRUE)
withoutint <- mixedmirt(data, covdata, model, fixed = ~ 0 + group, return.design = TRUE)

#notice that in result above, the intercepts 'items1 to items 10' were reassigned to 'd'
head(withint$X)
tail(withint$X)
head(withoutint$X) #no intercepts design here to be reassigned into item intercepts
tail(withoutint$X)

#####
### random effects
#make the number of groups much larger
covdata$group <- factor(rep(paste0('G',1:50), each = N/50))

#random groups
rmod1 <- mixedmirt(data, covdata, 1, fixed = ~ 0 + items, random = ~ 1|group)
summary(rmod1)
coef(rmod1)

#random groups and random items
rmod2 <- mixedmirt(data, covdata, 1, random = list(~ 1|group, ~ 1|items))
summary(rmod2)
eff <- randef(rmod2) #estimate random effects

#random slopes with fixed intercepts (suppressed correlation)
rmod3 <- mixedmirt(data, covdata, 1, fixed = ~ 0 + items, random = ~ -1 + pseudoIQ|group)
summary(rmod3)
(eff <- randef(rmod3))

#####
##LLTM, and 2PL version of LLTM
data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
model <- mirt.model('Theta = 1-32')

```

```

# Suppose that the first 16 items were suspected to be easier than the last 16 items,
# and we wish to test this item structure hypothesis (more intercept designs are possible
# by including more columns).
itemdesign <- data.frame(itemorder = factor(c(rep('easier', 16), rep('harder', 16))))

#notice that the 'fixed = ~ ... + items' argument is omitted
LLTM <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemdesign = itemdesign,
  SE = TRUE) # SE argument ensures that the information matrix is computed accurately
summary(LLTM)
coef(LLTM)
wald(LLTM)
L <- matrix(c(-1, 1, 0), 1)
wald(LLTM, L) #first half different from second

#compare to items with estimated slopes (2PL)
twoPL <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemtype = '2PL',
  itemdesign = itemdesign)
#twoPL not mixing too well (AR should be between .2 and .5), decrease MHCand
twoPL <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemtype = '2PL',
  itemdesign = itemdesign, technical = list(MHCand = 0.8))
anova(twoPL, LLTM) #much better fit
summary(twoPL)
coef(twoPL)

wald(twoPL)
L <- matrix(0, 1, 34)
L[1, 1] <- 1
L[1, 2] <- -1
wald(twoPL, L) #n.s., which is the correct conclusion. Rasch approach gave wrong inference

##LLTM with item error term
LLTMwithError <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, random = ~ 1|items,
  itemdesign = itemdesign)
summary(LLTMwithError)
#large item level variance after itemorder is regressed; not a great predictor of item difficulty
coef(LLTMwithError)

#####
### Polytomous example

#make an arbitrary group difference
covdat <- data.frame(group = rep(c('m', 'f'), nrow(Science)/2))

#partial credit model
mod <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group)
coef(mod)

#gpcm to estimate slopes
mod2 <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group,
  itemtype = 'gpcm')
summary(mod2)
anova(mod, mod2)

```

```
#graded model
mod3 <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group,
                 itemtype = 'graded')
coef(mod3)

## End(Not run)
```

mod2values	<i>Convert an estimated mirt model to special data.frame</i>
------------	--

Description

Given an estimated model from any of mirt's model fitting functions this function will convert the model parameters into the design data frame of starting values and other parameter characteristics (similar to using the `pars = 'values'` for obtaining starting values).

Usage

```
mod2values(x)
```

Arguments

`x` an estimated model `x` from the mirt package

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)
values <- mod2values(mod)
values

#use the converted values as starting values in a new model
mod2 <- mirt(dat, 1, pars = values)

## End(Not run)
```

multipleGroup

*Multiple Group Estimation***Description**

multipleGroup performs a full-information maximum-likelihood multiple group analysis for any combination of dichotomous and polytomous data under the item response theory paradigm using either Cai's (2010) Metropolis-Hastings Robbins-Monro (MHRM) algorithm or with an EM algorithm approach. This function may be used for detecting differential item functioning (DIF), though the [DIF](#) function may provide a more convenient approach.

Usage

```
multipleGroup(data, model, group, invariance = "", method = "EM", ...)
```

Arguments

data	a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
model	a single model object returned from <code>mirt.model()</code> declaring how the factor model is to be estimated. See mirt.model for more details
group	a character vector indicating group membership
invariance	a character vector containing the following possible options: 'free_means' for freely estimating all latent means (reference group constrained to 0) 'free_var' for freely estimating all latent variances (reference group constrained to 1's) 'free_cov' for freely estimating all latent covariances (reference group constrained to an Identity matrix) 'free_varcov' calls both 'free_var' and 'free_cov' 'slopes' to constrain all the slopes to be equal across all groups 'intercepts' to constrain all the intercepts to be equal across all groups, note for nominal models this also includes the category specific slope parameters Additionally, specifying specific item name bundles (from <code>colnames(data)</code>) will constrain all freely estimated parameters in each item to be equal across groups. This is useful for selecting 'anchor' items for vertical and horizontal scaling, and for detecting differential item functioning (DIF) across groups
method	a character object specifying the estimation algorithm to be used. The default is 'EM', for the standard EM algorithm with fixed quadrature. The option 'MHRM' may also be passed to use the MH-RM algorithm
...	additional arguments to be passed to the estimation engine. See mirt for details and examples

Details

By default the estimation in `multipleGroup` assumes that the models are maximally independent, and therefore could initially be performed by sub-setting the data and running identical models with `mirt` and aggregating the results (e.g., log-likelihood). However, constraints may be automatically imposed across groups by invoking various invariance keywords. Users may also supply a list of parameter equality constraints to by `constrain` argument, or define equality constraints using the `mirt.model` syntax (recommended).

Value

function returns an object of class `MultipleGroupClass` ([MultipleGroupClass-class](#)).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

See Also

[mirt](#), [DIF](#), [extract.group](#)

Examples

```
## Not run:
#single factor
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('dich', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
models <- mirt.model('F1 = 1-15')

mod_configural <- multipleGroup(dat, models, group = group) #completely separate analyses
#limited information fit statistics
M2(mod_configural)

mod_metric <- multipleGroup(dat, models, group = group, invariance=c('slopes')) #equal slopes
#equal intercepts, free variance and means
mod_scalar2 <- multipleGroup(dat, models, group = group,
                             invariance=c('slopes', 'intercepts', 'free_var','free_means'))
mod_scalar1 <- multipleGroup(dat, models, group = group, #fixed means
                             invariance=c('slopes', 'intercepts', 'free_var'))
mod_fullconstrain <- multipleGroup(dat, models, group = group,
                                   invariance=c('slopes', 'intercepts'))
slot(mod_fullconstrain, 'time') #time of estimation components

#optionally use Newton-Raphson for (generally) faster convergence in the M-step's
mod_fullconstrain <- multipleGroup(dat, models, group = group, optimizer = 'NR',
```

```

                                invariance=c('slopes', 'intercepts'))
slot(mod_fullconstrain, 'time') #time of estimation componenets

summary(mod_scalar2)
coef(mod_scalar2)
residuals(mod_scalar2)
plot(mod_configural)
plot(mod_configural, type = 'score')
plot(mod_configural, type = 'trace')
plot(mod_configural, type = 'trace', which.items = 1:4)
itemplot(mod_configural, 2)
itemplot(mod_configural, 2, type = 'RE')

anova(mod_metric, mod_configural) #equal slopes only
anova(mod_scalar2, mod_metric) #equal intercepts, free variance and mean
anova(mod_scalar1, mod_scalar2) #fix mean
anova(mod_fullconstrain, mod_scalar1) #fix variance

#test whether first 6 slopes should be equal across groups
values <- multipleGroup(dat, models, group = group, pars = 'values')
values
constrain <- list(c(1, 63), c(5,67), c(9,71), c(13,75), c(17,79), c(21,83))
equalslopes <- multipleGroup(dat, models, group = group, constrain = constrain)
anova(equalslopes, mod_configural)

#same as above, but using mirt.model syntax
newmodel <- mirt.model('
  F = 1-15
  CONSTRAINB = (1-6, a1)')
equalslopes <- multipleGroup(dat, newmodel, group = group)
coef(equalslopes)

#####
#DIF test for each item (using all other items as anchors)
itemnames <- colnames(dat)
refmodel <- multipleGroup(dat, models, group = group, SE=TRUE,
                          invariance=c('free_means', 'free_varcov', itemnames))

#loop over items (in practice, run in parallel to increase speed). May be better to use ?DIF
estmodels <- vector('list', ncol(dat))
for(i in 1:ncol(dat))
  estmodels[[i]] <- multipleGroup(dat, models, group = group, verbose = FALSE, calcNull=FALSE,
                                invariance=c('free_means', 'free_varcov', itemnames[-i]))

(anovas <- lapply(estmodels, anova, object2=refmodel, verbose=FALSE))

#family-wise error control
p <- do.call(rbind, lapply(anovas, function(x) x[2, 'p']))
p.adjust(p, method = 'BH')

#same as above, except only test if slopes vary (1 df)
#constrain all intercepts

```

```

estmodels <- vector('list', ncol(dat))
for(i in 1:ncol(dat))
  estmodels[[i]] <- multipleGroup(dat, models, group = group, verbose = FALSE, calcNull=FALSE,
                                invariance=c('free_means', 'free_varcov', 'intercepts',
                                itemnames[-i]))

(anovas <- lapply(estmodels, anova, object2=refmodel, verbose=FALSE))

#quickly test with Wald test using DIF()
mod_configural2 <- multipleGroup(dat, models, group = group, SE=TRUE)
DIF(mod_configural2, which.par = c('a1', 'd'), Wald=TRUE, p.adjust = 'fdr')

#####
#multiple factors

a <- matrix(c(abs(rnorm(5,1,.3)), rep(0,15),abs(rnorm(5,1,.3)),
rep(0,15),abs(rnorm(5,1,.3))), 15, 3)
d <- matrix(rnorm(15,0,.7),ncol=1)
mu <- c(-.4, -.7, .1)
sigma <- matrix(c(1.21,.297,1.232,.297,.81,.252,1.232,.252,1.96),3,3)
itemtype <- rep('dich', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = mu, sigma = sigma)
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))

#group models
model <- mirt.model('
  F1 = 1-5
  F2 = 6-10
  F3 = 11-15')

#define mirt cluster to use parallel architecture
mirtCluster()

#EM approach (not as accurate with 3 factors, but generally good for quick model comparisons)
mod_configural <- multipleGroup(dat, model, group = group) #completely separate analyses
mod_metric <- multipleGroup(dat, model, group = group, invariance=c('slopes')) #equal slopes
mod_fullconstrain <- multipleGroup(dat, model, group = group, #equal means, slopes, intercepts
                                invariance=c('slopes', 'intercepts'))

anova(mod_metric, mod_configural)
anova(mod_fullconstrain, mod_metric)

#same as above, but with MHRM (generally more accurate with 3+ factors, but slower)
mod_configural <- multipleGroup(dat, model, group = group, method = 'MHRM')
mod_metric <- multipleGroup(dat, model, group = group, invariance=c('slopes'), method = 'MHRM')
mod_fullconstrain <- multipleGroup(dat, model, group = group, method = 'MHRM',
                                invariance=c('slopes', 'intercepts'))

anova(mod_metric, mod_configural)
anova(mod_fullconstrain, mod_metric)

```

```
#####
#polytomous item example
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
d <- cbind(d, d-1, d-2)
itemtype <- rep('graded', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
model <- mirt.model('F1 = 1-15')

mod_configural <- multipleGroup(dat, model, group = group)
plot(mod_configural)
plot(mod_configural, type = 'SE')
itemplot(mod_configural, 1)
itemplot(mod_configural, 1, type = 'info')
fs <- fscores(mod_configural)
head(fs[["D1"]])
fscores(mod_configural, method = 'EAPsum')

# constrain slopes within each group to be equal (but not across groups)
model2 <- mirt.model('F1 = 1-15
                     CONSTRAIN = (1-15, a1)')
mod_configural2 <- multipleGroup(dat, model2, group = group)
plot(mod_configural2, type = 'SE')
plot(mod_configural2, type = 'RE')
itemplot(mod_configural2, 10)

#####
## empirical histogram example (normal and bimodal groups)
set.seed(1234)
a <- matrix(rlnorm(50, .2, .2))
d <- matrix(rnorm(50))
ThetaNormal <- matrix(rnorm(2000))
ThetaBimodal <- scale(matrix(c(rnorm(1000, -2), rnorm(1000,2)))) #bimodal
Theta <- rbind(ThetaNormal, ThetaBimodal)
dat <- simdata(a, d, 4000, itemtype = 'dich', Theta=Theta)
group <- rep(c('G1', 'G2'), each=2000)

EH <- multipleGroup(dat, 1, group=group, empiricalhist = TRUE, invariance = colnames(dat))
coef(EH)
plot(EH, type = 'empiricalhist', npts = 60)

#dif test for item 1
EH1 <- multipleGroup(dat, 1, group=group, empiricalhist = TRUE, invariance = colnames(dat)[-1])
anova(EH, EH1)

## End(Not run)
```

MultipleGroupClass-class
Class "MultipleGroupClass"

Description

Defines the object returned from `multipleGroup`.

Slots

iter: Object of class "numeric", number of iterations
pars: Object of class "list", estimated parameter objects list
shortpars: Object of class "numeric", unique estimated parameters
model: Object of class "list", list containing original model
K: Object of class "numeric", number of item categories
itemloc: Object of class "numeric", index for tabdata
df: Object of class "numeric", degrees of freedom
AIC: Object of class "numeric", Akaike's information criteria
BIC: Object of class "numeric", Bayesian information criteria
G2: Object of class "numeric", G squared stat
p: Object of class "numeric", p-value for G2
df: Object of class "numeric", degrees of freedom
RMSEA: Object of class "numeric", root mean-square error of approximation for G2
TLI: Object of class "numeric", Tucker-Lewis index for G2
CFI: Object of class "numeric", CFI for G2
logLik: Object of class "numeric", observed log-likelihood
SElogLik: Object of class "numeric", Monte Carlo standard error for log-likelihood
Prior: Object of class "numeric", prior distribution used during estimation. Empty unless `empiricalhist = TRUE`
F: Object of class "matrix", unrotated factor loadings
h2: Object of class "numeric", commonalities
Theta: Object of class "matrix", ability grid
Pl: Object of class "numeric", normed likelihoods for tabulated response
prodlist: Object of class "list", list containing product combination of factors
converge: Object of class "numeric", convergence diagnostic
quadpts: Object of class "numeric", number of quadrature points
esttype: Object of class "character", indicates whether estimation was 'EM' or 'MHRM'
constrain: Object of class "list", list of constraints
invariance: Object of class "character", invariance input

null.mod: Object of class "ExploratoryClass", null model
condnum: Object of class "numeric", condition number of information matrix
bfactor: Object of class "list", contains information from bfactor() estimation
secondordertest: Object of class "logical", indicate whether information matrix passes second-order test
infomethod: Object of class "character", indicates which information estimation method was used
TOL: Object of class "numeric", tolerance stopping criteria
CUSTOM.IND: Object of class "integer", an internal index
SLOW.IND: Object of class "integer", an internal index
Call: Object of class "call", call

Methods

coef signature(object = "MultipleGroupClass")
print signature(x = "MultipleGroupClass")
show signature(object = "MultipleGroupClass")
anova signature(object = "MultipleGroupClass")

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

personfit

Person fit statistics

Description

personfit calculates the Zh values from Drasgow, Levine and Williams (1985) for unidimensional and multidimensional models. For Rasch models infit and outfit statistics are also produced. The returned object is a data.frame consisting either of the tabulated data or full data with the statistics appended to the rightmost columns.

Usage

```
personfit(x, method = "EAP", Theta = NULL, stats.only = TRUE, ...)
```

Arguments

x	a computed model object of class ExploratoryClass, ConfirmatoryClass, or MultipleGroupClass
method	type of factor score estimation method. See fscores for more detail
Theta	a matrix of factor scores used for statistics that require empirical estimates. If supplied, arguments typically passed to <code>fscores()</code> will be ignored and these values will be used instead
stats.only	logical; return only the person fit statistics without their associated response pattern?
...	additional arguments to be passed to <code>fscores()</code>

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Dragow, F., Levine, M. V., & Williams, E. A. (1985). Appropriateness measurement with polychotomous item response models and standardized indices. *Journal of Mathematical and Statistical Psychology*, 38, 67-86.

Reise, S. P. (1990). A comparison of item- and person-fit methods of assessing model-data fit in IRT. *Applied Psychological Measurement*, 14, 127-137.

Wright B. D. & Masters, G. N. (1982). *Rating scale analysis*. MESA Press.

See Also

[itemfit](#)

Examples

```
## Not run:

#make some data
set.seed(1234)
a <- matrix(rlnorm(20),ncol=1)
d <- matrix(rnorm(20),ncol=1)
items <- rep('dich', 20)
data <- simdata(a,d, 2000, items)

x <- mirt(data, 1)
fit <- personfit(x)
head(fit)

#using precomputed Theta
Theta <- fscores(x, method = 'MAP', full.scores = TRUE)
personfit(x, Theta=Theta)

#multiple group Rasch model example
set.seed(12345)
```

```

a <- matrix(rep(1, 15), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('dich', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
MGmodel1 <- 'F1 = 1-15'
models <- mirt.model(MGmodel1, quiet = TRUE)
mod_Rasch <- multipleGroup(dat, models, itemtype = 'Rasch', group = group)
coef(mod_Rasch)
pf <- personfit(mod_Rasch, method='MAP')
head(pf)

## End(Not run)

```

PLCI.mirt

Compute profiled-likelihood confidence intervals

Description

Computes profiled-likelihood based confidence intervals. Supports the inclusion of prior parameter distributions as well as equality constraints.

Usage

```
PLCI.mirt(mod, alpha = 0.05, parnum = NULL)
```

Arguments

mod	a converged mirt model
alpha	two-tailed alpha critical level
parnum	a numeric vector indicating which parameters to estimate. Use mod2values to determine parameter numbers. If NULL, all possible parameters are used

See Also

[boot.mirt](#)

Examples

```

## Not run:
mirtCluster() #use all available cores to estimate CI's in parallel
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)

result <- PLCI.mirt(mod)

```



```

result

mod2 <- mirt(Science, 1)
result2 <- PLCI.mirt(mod2)
result2

#only estimate CI's slopes
sv <- mod2values(mod2)
parnum <- sv$parnum[sv$name == 'a1']
result3 <- PLCI.mirt(mod2, parnum=parnum)
result3

## End(Not run)

```

plot-method

Plot various test implied functions from models

Description

Plot various test implied response functions from models estimated in the mirt package.

Usage

```

## S4 method for signature 'ExploratoryClass,missing'
plot(x, y, type = "info", npts = 50,
     theta_angle = 45, theta_lim = c(-6, 6),
     which.items = 1:ncol(x@Data$data), MI = 0, CI = 0.95, rot = list(xaxis
     = -70, yaxis = 30, zaxis = 10), facet_items = TRUE, auto.key = TRUE,
     main = NULL, drape = TRUE, colorkey = TRUE, ehist.cut = 1e-10,
     add.ylab2 = TRUE, ...)

```

Arguments

x	an object of class ExploratoryClass, ConfirmatoryClass or MultipleGroupClass
y	an arbitrary missing argument required for R CMD check
type	type of plot to view; can be 'info' to show the test information function, 'infocontour' for the test information contours, 'SE' for the test standard error function, 'trace' and 'infotrace' for all item probability information or trace lines (only available when all items are dichotomous), 'infoSE' for a combined test information and standard error plot, and 'score' and 'scorecontour' for the expected total score surface and contour plots. If empiricalhist = TRUE was used in estimation then the type 'empiricalhist' also will be available to generate the empirical histogram plot
theta_angle	numeric values ranging from 0 to 90 used in plot. If a vector is used then a bubble plot is created with the summed information across the angles specified (e.g., theta_angle = seq(0, 90, by=10))

theta_lim	lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with npts
npts	number of quadrature points to be used for plotting features. Larger values make plots look smoother
MI	a single number indicating how many imputations to draw to form bootstrapped confidence intervals for the selected test statistic. If greater than 0 a plot will be drawn with a shaded region for the interval
CI	a number from 0 to 1 indicating the confidence interval to select when MI input is used. Default uses the 95% confidence (CI = .95)
rot	allows rotation of the 3D graphics
which.items	numeric vector indicating which items to be used when plotting. Default is to use all available items
facet.items	logical; apply grid of plots across items? If FALSE, items will be placed in one plot for each group
auto.key	logical parameter passed to the lattice package
ehist.cut	a probability value indicating a threshold for excluding cases in empirical histogram plots. Values larger than the default will include more points in the tails of the plot, potentially squishing the 'meat' of the plot to take up less area than visually desired
main	argument passed to lattice. Default generated automatically
drape	logical argument passed to lattice. Default generated automatically
colorkey	logical argument passed to lattice. Default generated automatically
add.ylab2	logical argument passed to lattice. Default generated automatically
...	additional arguments to be passed to lattice

Examples

```
## Not run:
x <- mirt(Science, 1, SE=TRUE)
plot(x)
plot(x, type = 'trace')
plot(x, type = 'infotrace')
plot(x, type = 'infotrace', facet.items = FALSE)
plot(x, type = 'infoSE')

# confidence interval plots when information matrix computed
plot(x, type='score')
plot(x, type='score', MI=100)
plot(x, type='info', MI=100)
plot(x, type='SE', MI=100)

set.seed(1234)
group <- sample(c('g1','g2'), nrow(Science), TRUE)
x2 <- multipleGroup(Science, 1, group)
plot(x2)
plot(x2, type = 'trace')
```

```
plot(x2, type = 'trace', which.items = 1:2)
plot(x2, type = 'trace', which.items = 1, facet_items = FALSE) #facet by group
plot(x2, type = 'score')

x3 <- mirt(Science, 2)
plot(x3)
plot(x3, type = 'SE')

## End(Not run)
```

print-method *Print the model objects*

Description

Print model object summaries to the console.

Usage

```
## S4 method for signature 'ExploratoryClass'
print(x)
```

Arguments

x an object of class ExploratoryClass, ConfirmatoryClass, MultipleGroupClass, or MixedClass

Examples

```
## Not run:
x <- mirt(Science, 1)
print(x)

## End(Not run)
```

probtrace *Function to calculate probability trace lines*

Description

Given an internal mirt object extracted from an estimated model compute the probability trace lines for all categories.

Usage

```
probtrace(x, Theta)
```

Arguments

`x` an extracted internal mirt object containing item information

`Theta` a vector (unidimensional) or matrix (unidimensional/multidimensional) of latent trait values

See Also

[extract.item](#)

Examples

```
## Not run:
mod <- mirt(Science, 1)
extr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-4,4, by = .1))
traceline <- probtrace(extr.2, Theta)

head(data.frame(traceline, Theta=Theta))

## End(Not run)
```

randef	<i>Compute random effects</i>
--------	-------------------------------

Description

Stochastically compute random effects for `MixedClass` objects with Metropolis-Hastings samplers and averaging over the draws. Returns a list of the estimated effects.

Usage

```
randef(x, ndraws = 1000, thin = 10)
```

Arguments

`x` an estimated model object from the [mixedmirt](#) function

`ndraws` total number of draws to perform. Default is 1000

`thin` amount of thinning to apply. Default is to use every 10th draw

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:
#make an arbitrary groups
covdat <- data.frame(group = rep(paste0('group', 1:49), each=nrow(Science)/49))

#partial credit model
mod <- mixedmirt(Science, covdat, model=1, random = ~ 1|group)
summary(mod)

effects <- randef(mod, ndraws = 2000, thin = 20)
head(effects$Theta)
head(effects$group)

## End(Not run)
```

read.mirt

Translate mirt parameters for plink package

Description

This function exports item parameters from the mirt package to the plink package.

Usage

```
read.mirt(x, as.irt.pars = TRUE, ...)
```

Arguments

x	an object returned from mirt, bfactor, or multipleGroup
as.irt.pars	if TRUE, the parameters will be output as an irt.pars object
...	additional arguments to be passed to coef()

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```
## Not run:

## unidimensional

data <- expand.table(LSAT7)
(mod1 <- mirt(data, 1))
plinkpars <- read.mirt(mod1)
plot(plinkpars)
itemplot(mod1, 1)
```

```
#graded
mod2 <- mirt(Science, 1)
plinkpars <- read.mirt(mod2)
plot(plinkpars)
itemplot(mod2, 1)

#gpcm
mod3 <- mirt(Science, 1, itemtype = 'gpcm')
plinkpars <- read.mirt(mod3)
plot(plinkpars)
itemplot(mod3, 1)

#nominal
mod4 <- mirt(Science, 1, itemtype = 'nominal')
plinkpars <- read.mirt(mod4)
plot(plinkpars)
itemplot(mod4, 1)

## multidimensional

data <- expand.table(LSAT7)
(mod1 <- mirt(data, 2))
plinkpars <- read.mirt(mod1)
plot(plinkpars)
itemplot(mod1, 1)

cmod <- mirt.model('
  F1 = 1,4,5
  F2 = 2-4')
model <- mirt(data, cmod)
plot(read.mirt(model))
itemplot(model, 1)

#graded
mod2 <- mirt(Science, 2)
plinkpars <- read.mirt(mod2)
plot(plinkpars)
itemplot(mod2, 1)

### multiple group
set.seed(1234)
dat <- expand.table(LSAT7)
group <- sample(c('g1', 'g2'), nrow(dat), TRUE)
mod <- multipleGroup(dat, 1, group)

# convert, and combine pars
plinkMG <- read.mirt(mod)
combine <- matrix(1:5, 5, 2)
comb <- combine.pars(plinkMG, combine, grp.names=unique(group))
out <- plink(comb, rescale="SL")
equate(out)
equate(out, method = 'OSE')
```

```
## End(Not run)
```

```
residuals-method      Compute model residuals
```

Description

Return model implied residuals for linear dependencies between items or at the person level.

Usage

```
## S4 method for signature 'ExploratoryClass'
residuals(object, type = "LD", digits = 3,
  df.p = FALSE, full.scores = FALSE, printvalue = NULL, tables = FALSE,
  verbose = TRUE, Theta = NULL, ...)
```

Arguments

object	an object of class ExploratoryClass, ConfirmatoryClass or MultipleGroupClass. Bifactor models are automatically detected and utilized for better accuracy
type	type of residuals to be displayed. Can be either 'LD' or 'LDG2' for a local dependence matrix based on the X2 or G2 statistics (Chen & Thissen, 1997), 'Q3' for the statistic proposed by Yen (1984), or 'exp' for the expected values for the frequencies of every response pattern
tables	logical; for LD type, return the observed, expected, and standardized residual tables for each item combination?
digits	number of significant digits to be rounded
df.p	logical; print the degrees of freedom and p-values?
full.scores	logical; compute relevant statistics for each subject in the original data?
printvalue	a numeric value to be specified when using the res='exp' option. Only prints patterns that have standardized residuals greater than abs(printvalue). The default (NULL) prints all response patterns
verbose	logical; allow information to be printed to the console?
Theta	a matrix of factor scores used for statistics that require empirical estimates (i.e., Q3). If supplied, arguments typically passed to fscores() will be ignored and these values will be used instead
...	additional arguments to be passed to fscores()

References

Chen, W. H. & Thissen, D. (1997). Local dependence indices for item pairs using item response theory. *Journal of Educational and Behavioral Statistics*, 22, 265-289.

Yen, W. (1984). Effects of local item dependence on the fit and equating performance of the three parameter logistic model. *Applied Psychological Measurement*, 8, 125-145.

Examples

```
## Not run:

x <- mirt(Science, 1)
residuals(x)
residuals(x, tables = TRUE)
residuals(x, type = 'exp')

# with and without supplied factor scores
Theta <- fscores(x, full.scores=TRUE, scores.only=TRUE)
residuals(x, type = 'Q3', Theta=Theta)
residuals(x, type = 'Q3', method = 'ML')

## End(Not run)
```

SAT12

*Description of SAT12 data***Description**

Data obtained from the TESTFACT (Woods et al., 2003) manual, with 32 response pattern scored items for a grade 12 science assessment test (SAT) measuring topics of chemistry, biology, and physics. The scoring key for these data is [1, 4, 5, 2, 3, 1, 2, 1, 3, 1, 2, 4, 2, 1, 5, 3, 4, 4, 1, 4, 3, 3, 4, 1, 3, 5, 1, 3, 1, 5, 4, 5], respectively. However, careful analysis using the nominal response model suggests that the scoring key for item 32 may be incorrect, and should be changed from 5 to 3.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Wood, R., Wilson, D. T., Gibbons, R. D., Schilling, S. G., Muraki, E., & Bock, R. D. (2003). TESTFACT 4 for Windows: Test Scoring, Item Statistics, and Full-information Item Factor Analysis [Computer software]. Lincolnwood, IL: Scientific Software International.

Examples

```
## Not run:
#score the data (missing scored as 0)
head(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

#score the data, missing treated as NA
SAT12missing <- SAT12
SAT12missing[SAT12missing == '8'] <- NA
data <- key2binary(SAT12missing,
```



```

key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

#potentially better scoring for item 32
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,3))

## End(Not run)

```

Science	<i>Description of Science data</i>
---------	------------------------------------

Description

A 4-item data set borrowed from ltm package in R, first example of the grm() function. See more complete documentation therein.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

```

## Not run:
mod <- mirt(Science, 1)
plot(mod, type = 'trace')

## End(Not run)

```

show-method	<i>Show model object</i>
-------------	--------------------------

Description

Print model object summaries to the console.

Usage

```

## S4 method for signature 'ExploratoryClass'
show(object)

```

Arguments

object	an object of class ExploratoryClass, ConfirmatoryClass, MultipleGroupClass, or MixedClass
--------	---

Examples

```
## Not run:
x <- mirt(Science, 1)
show(x)

## End(Not run)
```

simdata

Simulate response patterns

Description

Simulates response patterns for compensatory and noncompensatory MIRT models from multivariate normally distributed factor (θ) scores, or from a user input matrix of θ 's.

Usage

```
simdata(a, d, N, itemtype, sigma = NULL, mu = NULL, guess = 0,
        upper = 1, nominal = NULL, Theta = NULL, returnList = FALSE)
```

Arguments

- | | |
|----------|--|
| a | a matrix of slope parameters. If slopes are to be constrained to zero then use NA. a may also be a similar matrix specifying factor loadings if <code>factor.loads = TRUE</code> |
| d | a matrix of intercepts. The matrix should have as many columns as the item with the largest number of categories, and filled empty locations with NA |
| itemtype | a character vector of length <code>nrow(a)</code> (or 1, if all the item types are the same) specifying the type of items to simulate.
Can be 'dich', 'graded', 'gpcm', 'nominal', 'nestlogit', or 'partcomp', for dichotomous, graded, generalized partial credit, nominal, nested logit, and partially compensatory models. Note that for the gpcm, nominal, and nested logit models there should be as many parameters as desired categories, however to parametrize them for meaningful interpretation the first category intercept should equal 0 for these models (second column for 'nestlogit', since first column is for the correct item traseline). For nested logit models the 'correct' category is always the lowest category (i.e., == 1). It may be helpful to use mod2values on data-sets that have already been estimated to understand the itemtypes more intimately |
| nominal | a matrix of specific item category slopes for nominal models. Should be the dimensions as the intercept specification with one less column, with NA in locations where not applicable. Note that during estimation the first slope will be constrained to 0 and the last will be constrained to the number of categories minus 1, so it is best to set these as the values for the first and last categories as well |
| N | sample size |

guess	a vector of guessing parameters for each item; only applicable for dichotomous items. Must be either a scalar value that will affect all of the dichotomous items, or a vector with as many values as to be simulated items
upper	same as guess, but for upper bound parameters
sigma	a covariance matrix of the underlying distribution. Default is the identity matrix
mu	a mean vector of the underlying distribution. Default is a vector of zeros
Theta	a user specified matrix of the underlying ability parameters, where $nrow(\text{Theta}) == N$ and $ncol(\text{Theta}) == ncol(a)$
returnList	logical; return a list containing the data, item objects defined by <code>mirt</code> containing the population parameters and item structure, and the latent trait matrix <code>Theta</code> ? Default is FALSE

Details

Returns a data matrix simulated from the parameters, or a list containing the data, item objects, and Theta matrix.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Reckase, M. D. (2009). *Multidimensional Item Response Theory*. New York: Springer.

Examples

```
## Not run:
###Parameters from Reckase (2009), p. 153

set.seed(1234)

a <- matrix(c(
  .7471, .0250, .1428,
  .4595, .0097, .0692,
  .8613, .0067, .4040,
  1.0141, .0080, .0470,
  .5521, .0204, .1482,
  1.3547, .0064, .5362,
  1.3761, .0861, .4676,
  .8525, .0383, .2574,
  1.0113, .0055, .2024,
  .9212, .0119, .3044,
  .0026, .0119, .8036,
  .0008, .1905, 1.1945,
  .0575, .0853, .7077,
  .0182, .3307, 2.1414,
  .0256, .0478, .8551,
  .0246, .1496, .9348,
  .0262, .2872, 1.3561,
```

```

.0038, .2229, .8993,
.0039, .4720, .7318,
.0068, .0949, .6416,
.3073, .9704, .0031,
.1819, .4980, .0020,
.4115,1.1136, .2008,
.1536,1.7251, .0345,
.1530, .6688, .0020,
.2890,1.2419, .0220,
.1341,1.4882, .0050,
.0524, .4754, .0012,
.2139, .4612, .0063,
.1761,1.1200, .0870),30,3,byrow=TRUE)*1.702

d <- matrix(c(.1826,-.1924,-.4656,-.4336,-.4428,-.5845,-1.0403,
.6431,.0122,.0912,.8082,-.1867,.4533,-1.8398,.4139,
-.3004,-.1824,.5125,1.1342,.0230,.6172,-.1955,-.3668,
-1.7590,-.2434,.4925,-.3410,.2896,.006,.0329),ncol=1)*1.702

mu <- c(-.4, -.7, .1)
sigma <- matrix(c(1.21,.297,1.232,.297,.81,.252,1.232,.252,1.96),3,3)

dataset1 <- simdata(a, d, 2000, itemtype = 'dich')
dataset2 <- simdata(a, d, 2000, itemtype = 'dich', mu = mu, sigma = sigma)

#mod <- mirt(dataset1, 3, method = 'MHRM')
#coef(mod)

###An example of a mixed item, bifactor loadings pattern with correlated specific factors

a <- matrix(c(
.8,.4,NA,
.4,.4,NA,
.7,.4,NA,
.8,NA,.4,
.4,NA,.4,
.7,NA,.4),ncol=3,byrow=TRUE)

d <- matrix(c(
-1.0,NA,NA,
1.5,NA,NA,
0.0,NA,NA,
0.0,-1.0,1.5, #the first 0 here is the recommended constraint for nominal
0.0,1.0,-1, #the first 0 here is the recommended constraint for gpcm
2.0,0.0,NA),ncol=3,byrow=TRUE)

nominal <- matrix(NA, nrow(d), ncol(d))
#the first 0 and last (ncat - 1) = 2 values are the recommended constraints
nominal[4, ] <- c(0,1.2,2)

sigma <- diag(3)
sigma[2,3] <- sigma[3,2] <- .25
items <- c('dich','dich','dich','nominal','gpcm','graded')
```

```

dataset <- simdata(a,d,2000,items,sigma=sigma,nominal=nominal)

#mod <- bfactor(dataset, c(1,1,1,2,2,2), itemtype=c(rep('2PL', 3), 'nominal', 'gpcm','graded'))
#coef(mod)

####Unidimensional nonlinear factor pattern

theta <- rnorm(2000)
Theta <- cbind(theta,theta^2)

a <- matrix(c(
.8,.4,
.4,.4,
.7,.4,
.8,NA,
.4,NA,
.7,NA),ncol=2,byrow=TRUE)
d <- matrix(rnorm(6))
itemtype <- rep('dich',6)

nonlindata <- simdata(a,d,2000,itemtype,Theta=Theta)

#model <- mirt.model('
#F1 = 1-6
#(F1 * F1) = 1-3')
#mod <- mirt(nonlindata, model)
#coef(mod)

####2PLNRM model for item 4 (with 4 categories), 2PL otherwise

a <- matrix(rlnorm(4,0,.2))

#first column of item 4 is the intercept for the correct category of 2PL model,
# otherwise nominal model configuration
d <- matrix(c(
-1.0,NA,NA,NA,
1.5,NA,NA,NA,
0.0,NA,NA,NA,
1, 0.0,-0.5,0.5),ncol=4,byrow=TRUE)

nominal <- matrix(NA, nrow(d), ncol(d))
nominal[4, ] <- c(NA,0,.5,.6)

items <- c(rep('dich',3),'nestlogit')

dataset <- simdata(a,d,2000,items,nominal=nominal)

#mod <- mirt(dataset, 1, itemtype = c('2PL', '2PL', '2PL', '2PLNRM'), key=c(NA,NA,NA,1))
#coef(mod)
#itemplot(mod,4)

#return list of simulation parameters

```

```
listobj <- simdata(a,d,2000,items,nominal=nominal, returnList=TRUE)
str(listobj)
```

```
## End(Not run)
```

summary-method

Summary of model object

Description

Transforms coefficients into a standardized factor loading's metric. For MixedClass objects, the fixed and random coefficients are printed.

Usage

```
## S4 method for signature 'ExploratoryClass'
summary(object, rotate = "", Target = NULL,
        suppress = 0, digits = 3, printCI = FALSE, verbose = TRUE, ...)
```

Arguments

object	an object of class ExploratoryClass, ConfirmatoryClass, MultipleGroupClass, or MixedClass
rotate	a string indicating which rotation to use for exploratory models, primarily from the GPARotation package (see documentation therein). Rotations currently supported are: 'promax', 'oblimin', 'varimax', 'quartimin', 'targetT', 'targetQ', 'pstT', 'pstQ', 'oblimax', 'entropy', 'quartimax', 'simplimax', 'bentlerT', 'bentlerQ', 'tandemI', 'tandemII', 'geominT', 'geominQ', 'cfT', 'cfQ', 'infomaxT', 'infomaxQ', 'mccammon', 'bifactorT', 'bifactorQ'
Target	a dummy variable matrix indicting a target rotation pattern
suppress	a numeric value indicating which (possibly rotated) factor loadings should be suppressed. Typical values are around .3 in most statistical software. Default is 0 for no suppression
printCI	print a confidence interval for standardized loadings (e.g., printCI = .95 gives a 95% confidence interval)
digits	number of significant digits to be rounded
verbose	logical; allow information to be printed to the console?
...	additional arguments to be passed

See Also

[coef-method](#)

Examples

```
## Not run:
x <- mirt(Science, 2)
summary(x)
summary(x, rotate = 'varimax')

#print confidence interval (requires computed information matrix)
x2 <- mirt(Science, 1, SE=TRUE)
summary(x2, printCI=.95)

## End(Not run)
```

testinfo

Function to calculate test information

Description

Given an estimated model compute the test information.

Usage

```
testinfo(x, Theta, degrees = NULL, group = NULL)
```

Arguments

x	an estimated mirt object
Theta	a matrix of latent trait values
degrees	a vector of angles in degrees that are between 0 and 90 that jointly sum to 90. Only applicable when the input object is multidimensional
group	a number signifying which group the item should be extracted from (applies to 'MultipleGroupClass' objects only)

Examples

```
## Not run:
dat <- expand.table(deAyala)
(mirt(dat, 1, '2PL', pars = 'values'))
mod <- mirt(dat, 1, '2PL', constrain = list(c(1,5,9,13,17)))

Theta <- matrix(seq(-4,4,.01))
tinfo <- testinfo(mod, Theta)
plot(Theta, tinfo, type = 'l')

#compare information loss between two tests
dat.smaller <- dat[,-c(1,2)]
mod2 <- mirt(dat.smaller, 1, '2PL', constrain = list(c(1,5,9)))
tinfo2 <- testinfo(mod2, Theta)
```

```
#removed item informations
plot(Theta, iteminfo(extract.item(mod, 1), Theta), type = 'l')
plot(Theta, iteminfo(extract.item(mod, 2), Theta), type = 'l')

#most loss of info around -1 when removing items 1 and 2; expected given item info functions
plot(Theta, tinfo2 - tinfo, type = 'l')

## End(Not run)
```

wald

Wald test for mirt models

Description

Compute a Wald test given an L vector or matrix of numeric contrasts. Requires that the model information matrix be computed (including SE = TRUE when using the EM method). Use `wald(model)` to observe how the information matrix columns are named, especially if the estimated model contains constrained parameters (e.g., 1PL).

Usage

```
wald(object, L, C = 0)
```

Arguments

L	a coefficient matrix with dimensions <code>nconstrasts x npars</code> . Omitting this value will return the column names of the information matrix used to identify the (potentially constrained) parameters
object	estimated object from <code>mirt</code> , <code>bfactor</code> , <code>multipleGroup</code> , or <code>mixedmirt</code>
C	a constant vector of population parameters to be compared along side L, where <code>length(C) == ncol(L)</code> . By default a vector of 0's is constructed

Examples

```
## Not run:
#View parnumber index
data(LSAT7)
data <- expand.table(LSAT7)
mod <- mirt(data, 1, SE = TRUE)
coef(mod)

# see how the information matrix relates to estimated parameters, and how it lines up
# with the parameter index
(infonames <- wald(mod))
index <- mod2values(mod)
index[index$est, ]
```



```
#second item slope equal to 0?
L <- matrix(0, 1, 10)
L[1,3] <- 1
wald(mod, L)

#simultaneously test equal factor slopes for item 1 and 2, and 4 and 5
L <- matrix(0, 2, 10)
L[1,1] <- L[2, 7] <- 1
L[1,3] <- L[2, 9] <- -1
L
wald(mod, L)

#logLikelihood tests (requires estimating a new model)
cmodel <- mirt.model('theta = 1-5
                    CONSTRAIN = (1,2, a1), (4,5, a1)')
mod2 <- mirt(data, cmodel)
#or, equivalently
#mod2 <- mirt(data, 1, constrain = list(c(1,5), c(13,17)))
anova(mod2, mod)

## End(Not run)
```

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